

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1471.46 Seconds
(without alignments)
10073.859 Million cell updates/sec

Title: US-10-027-725A-1
Perfect score: 342
Sequence: 1 ctgagctgtgcccaggact.....ccctgggtcacggtctctcca 342

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
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23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
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30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	340.4	99.5	342	9	HSA458382	AJ458382 Homo sapi
2	308.4	90.2	342	9	HSA458384	AJ458384 Homo sapi
3	297.2	86.9	342	9	HSA458383	AJ458383 Homo sapi
4	278.2	81.3	432	9	HSA419111	AJ491911 Homo sapi
5	277.2	81.1	411	9	HST22X1	Z75385 H.sapiens m
6	276.6	80.9	432	9	HSA451912	AJ491912 Homo sapi
7	276.4	80.8	351	9	HSA244930	AJ244930 Homo sapi
8	276.4	80.8	360	6	AX061463	AX061463 Sequence
9	275	80.4	414	9	AF062112	AF062112 Homo sapi
10	273.8	80.1	414	9	HST14X13	Z75365 H.sapiens m
11	273.8	80.1	414	9	HST14X4	Z75378 H.sapiens m
12	272	79.5	357	9	HSA244949	AJ244949 Homo sapi
13	271.8	79.5	354	9	HSA245064	AJ245064 Homo sapi
14	271.8	79.5	360	9	HSU80129	U80129 Human immun
15	271.8	79.5	360	9	HSU80130	U80130 Human immun
16	271.6	79.4	358	9	AF021954	AF021954 Homo sapi
17	270.6	79.1	403	12	AF452917	AF452917 Synthetic
18	270.4	79.1	363	9	HSU80131	U80131 Human immun
19	269.2	78.7	354	9	HSA244955	AJ244955 Homo sapi
20	269.2	78.7	417	9	HST14X9	Z75383 H.sapiens m
21	268.8	78.6	366	9	HSA233698	AJ233698 Homo sapi
22	268.6	78.5	351	9	HSA245020	AJ245020 Homo sapi
23	268.4	78.5	357	9	HSA279523	AJ279523 Homo sapi
24	267.4	78.2	400	12	AF452909	AF452909 Synthetic
25	266.8	78.0	357	9	HSA279541	AJ279541 Homo sapi
26	266.8	78.0	357	9	HSU80168	U80168 Human immun
27	266.2	77.8	412	12	AF452912	AF452912 Synthetic
28	265.8	77.7	366	9	HSA244928	AJ244928 Homo sapi
29	265.8	77.7	369	6	AX061433	AX061433 Sequence
30	265.6	77.7	363	9	HSU80128	U80128 Human immun
31	265.4	77.6	351	9	HSA244958	AJ244958 Homo sapi
32	265	77.5	362	9	HSU80169	U80169 Human immun
33	264	77.2	362	9	AF126269	AF126269 Homo sapi
34	263.8	77.1	351	9	HSA244953	AJ244953 Homo sapi
35	263.6	77.1	406	12	AF453047	AF453047 Synthetic
36	263.6	77.1	357	9	HSA279538	AJ279538 Homo sapi
37	263.4	77.0	362	9	HSU80166	U80166 Human immun
38	263.2	77.0	406	12	AF453217	AF453217 Synthetic
39	262.6	76.8	366	9	HSA279551	AJ279551 Homo sapi
40	262.4	76.7	409	12	AF452947	AF452947 Synthetic
41	262	76.6	357	9	HSA244964	AJ244964 Homo sapi
42	262	76.6	360	9	AB063905	AB063905 Homo sapi
43	261.2	76.4	361	9	HSA279518	AJ279518 Homo sapi
44	261	76.3	366	9	HSA244976	AJ244976 Homo sapi
45	261	76.3	366	9	HSU80111	U80111 Human immun

ALIGNMENTS

RESULT 1
HSA458382
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 94.
ACCESSION AJ458382
VERSION AJ458382.1 GI:20387063
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y., Valent P., Kraft D. and Valenta R.

Pred. No. is the number of results predicted by chance to have a

TITLE Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 342)
AUTHORS Flicker,S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 30, Wahringer Guertel 18-20, A-1090
Vienna, AUSTRIA

FEATURES
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Location/Qualifiers
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/db_xref="EMBL:CAD30444"
/translation="LESGPLVKPQATLSLCAVSGGSIRGGYVWSWIROPKGLKLE
WIGYVHSGNTYVNPFLSKRSRTAMSDTSENKFLRLNSVTAADTAVYYCARLDGVTLLD
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V_region

ORIGIN

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Best Local Similarity 99.7%; Pred. No. 1.1e-84;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTCCCTCAGCTGGCGCTGTC 60
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QY 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCGGCCAACACCCAGGG 120
Db 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCGGCCAACACCCAGGG 120

QY 121 AAGGCCCTGGAGTGGGTACATCTATCAGTGGGAACACCTACAGAACCCGCTCC 180
Db 121 AAGGCCCTGGAGTGGGTACATCTATCAGTGGGAACACCTACAGAACCCGCTCC 180

QY 181 CTCAGAGTCCGAGTGGGTACATCTATCAGTGGGAACACCTACAGAACCCGCTCC 240
Db 181 CTCAGAGTCCGAGTGGGTACATCTATCAGTGGGAACACCTACAGAACCCGCTCC 240

QY 241 AACTCTGTGACTGCCCGGACACCGCGGTATTACTGTGCGAGTTAGATGGCTACCT 300
Db 241 AACTCTGTGACTGCCCGGACACCGCGGTATTACTGTGCGAGTTAGATGGCTACCT 300

QY 301 TTGGACATCTGGGGCCAGGACCCCTGGTCACCGCTCTCTCA 342
Db 301 TTGGACATCTGGGGCCAGGACCCCTGGTCACCGCTCTCTCA 342

RESULT 2
HSA458384 342 bp mRNA linear PRI 30-APR-2002
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable
region (IGHV gene), clone 100.
ACCESSION AJ458384
VERSION AJ458384.1 GI:20387067
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
Valent,P., Kraft,D. and Valenta,R.
Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
2 (bases 1 to 342)
AUTHORS Flicker,S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 30, Wahringer Guertel 18-20, A-1090
Vienna, AUSTRIA

FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="100"
/rearranged
1..342
/gene="IGHV"
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/gene="IGHV"
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="CAD30446.1"
/db_xref="GI:20387068"
/db_xref="EMBL:CAD30446"
/translation="LESGPLVKPQATLSLCTVSGGSIRGGYVWSWIROPKGLKLE
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NWGGTLLVTSS"
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/gene="IGHV"
/product="immunoglobulin heavy chain variable region"

V_region

ORIGIN

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Best Local Similarity 93.9%; Pred. No. 1e-75;
Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTCCCTCAGCTGGCGCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCCCTCCCTCAGCTGGCGCTGTC 60

QY 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCGGCCAACACCCAGGG 120
Db 61 TCTGCGGCTCCATCCGAGTGGTGTACTACTCGAGTTGGATCGGCCAACCCAGGG 120

QY 121 AAGGCCCTGGAGTGGGTACATCTATCAGTGGGAACACCTACAGAACCCGCTCC 180
Db 121 AAGGCCCTGGAGTGGGTACATCTATCAGTGGGAACACCTACAGAACCCGCTCC 180

QY 181 CTCAGAGTCCGAGTGGGTACATCTATCAGTGGGAACACCTACAGAACCCGCTCC 240
Db 181 CTCAGAGTCCGAGTGGGTACATCTATCAGTGGGAACACCTACAGAACCCGCTCC 240

QY 241 AACTCTGTGACTGCCCGGACACCGCGGTATTACTGTGCGAGTTAGATGGCTACCT 300
Db 241 AACTCTGTGACTGCCCGGACACCGCGGTATTACTGTGCGAGTTAGATGGCTACCT 300

QY 301 TTGGACATCTGGGGCCAGGACCCCTGGTCACCGCTCTCTCA 342
Db 301 TTGGACATCTGGGGCCAGGACCCCTGGTCACCGCTCTCTCA 342

RESULT 3
HSA458383 342 bp mRNA linear PRI 30-APR-2002
LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable
region (IGHV gene), clone 60.
ACCESSION AJ458383
VERSION AJ458383.1 GI:20387065

KEYWORDS	IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y., Valent P., Kraft D. and Valenta R.
TITLE	Conversion of grass allergen-specific human IgE into a protective IgG1 antibody
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 342)
AUTHORS	Flicker S.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090 Vienna, AUSTRIA
FEATURES	Location/Qualifiers
source	1. .342 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="60" /rearranged 1. .342 /gene="IGHV" 1. .342 /gene="IGHV" 1. .342 /gene="IGHV" /product="immunoglobulin heavy chain"
gene	1. .342 /gene="IGHV"
CDS	1. .342 /gene="IGHV" /product="immunoglobulin heavy chain variable region"
V_region	1. .342 /gene="IGHV" /product="immunoglobulin heavy chain variable region"
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Query Match	86.9%; Score 297.2; DB 9; Length 342;
Best Local Similarity	91.8%; Pred. No. 1.5e-72;
Matches	314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY	1 CTCAGTCTGGCCAGACTGGTGAAGCCCTGCACAGACCTGTCCTCCCTCAGCTGCGTGTG 60
Db	1 CTCAGTCTGGCCAGACTGGTGAAGCCCTGCACAGACCTGTCCTCCCTCAGCTGCGTGTG 60
QY	61 TCTGGCGCTCCATCCGACGTGGTGTACTACTGGAGTTGGATCCGCCAACCCAGGG 120
Db	61 TCTGGTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGGTCCGCCAGCTCCAGGG 120
QY	121 AAGGCGCTGGAGTGGATTGGGTATCATCTATCACAGTGGGAACACCTACAAACACCCGTCC 180
Db	121 AAGGCGCTGGAGTGGATCGGCACATCTATCACAGTGGCACACCTACTACACCCGTCC 180
QY	181 CTCAGAGTCAATTCGATCGGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGCGTG 240
Db	181 CTCAGAGTCAATTCGATCGGTAGACACGCTCTGAGAACCACTTCTCCCTGAGACTG 240
QY	241 AACTCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGTTAGATGGCTACAT 300
Db	241 AACTCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGTTAGATGGCTACAT 300
QY	301 TTGACATCTCTGGGCGCAGGGAACCTGGTCAACCGTCTCCCTCA 342
Db	301 TTGACAACTCTGGGCGCAGGGAACCTGGTCAACCGTCTCCCTCA 342
RESULT 4	
HSA491911	81.3%; Score 278.2; DB 9; Length 432;
LOCUS	Best Local Similarity 88.8%; Pred. No. 3.2e-67;
DEFINITION	Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region (clone HD17 C9).
ACCESSION	AF491911
VERSION	AF491911.1 GI:24415808
KEYWORDS	constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1
AUTHORS	Coker H.A., Durham S.R. and Gould H.J.
TITLE	Local somatic hypermutation and class switch recombination in the nasal mucosa of allergic rhinitis patients
JOURNAL	J. Immunol. 171 (10), 5602-5610 (2003)
MEDLINE	22970235
PUBMED	14607969
REFERENCE	2 (bases 1 to 432)
AUTHORS	Coker H.A.
TITLE	Direct Submission
JOURNAL	Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall Centre, King's College London, Guy's Campus, London, SE1 1UL, UNITED KINGDOM
FEATURES	Location/Qualifiers
source	1. .432 /organism="Homo sapiens" /mol_type="mRNA" /isolation_source="nasal biopsy from inferior turbinate of allergic rhinitis patient" /db_xref="taxon:9606" /clone="HD17 C9" /sex="female" /cell_type="B lymphocyte" /tissue_type="nasal mucosa" /dev_stage="adult" /rearranged /country="United Kingdom" 1. .432 /gene="IGH" 1. .432 /gene="IGH" /codon_start=1 /product="immunoglobulin heavy chain V-D-J-Ce region" /protein_id="CAD38020.1" /db_xref="GI:24415809" /db_xref="REMBL:CAD38020" /translation="QVQLQSGPLVKPSQNLSTCTVSGAISGGYVMSWIRQHPG KGLEMTGYTYRGSTYYPNPSLRITMSIDTSANQFSRLTSLTAADTAVYFCARLDG YSLDYWGQGTLLTVSSASTQSPSVFPLTRCKNIPSNATSVT"
gene	1. .355 /gene="IGHV4-30"
V_region	1. .355 /gene="IGHV4-30" /product="immunoglobulin heavy chain variable region"
V_segment	1. .297 /gene="IGHV4-30" /note="VH segment"
D_segment	298. .315 /gene="IGHV4-30" /note="DS-24 rf 3"
J_segment	316. .355 /gene="IGHV4-30" /note="region JH4b"
gene	356. .432 /gene="IGHE"
C_region	356. .432 /gene="IGHE" /product="immunoglobulin epsilon heavy chain constant region"
ORIGIN	
Query Match	81.3%; Score 278.2; DB 9; Length 432;
Best Local Similarity	88.8%; Pred. No. 3.2e-67;

Matches 301; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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 Db 16 GAGTGGGCCCCAGGACTGGTGAAGCCTTTCACAGAACCTGTCCCTCACCTGCAGTGTCT 75
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 QY 64 GCGGCTCCATCCGCGAGTGGTGTACTACTGGAGTTGGATCCGCGCAACACCCAGGGAAG 123
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 Db 76 GGTGGCGCCATCAGTAGTGTGTACTACTGGAGTGGATCCGCGCAGCACCCAGGGAAG 135
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 QY 124 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAAACACTTACAAACCCCGTCCCTC 183
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 Db 136 GGCCTGGAGTGGATGGGATCACTATTTACAGGGGAGCAGCTACTACAAACCCGTCCTC 195
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 QY 184 AAGAGTCCAAATGCCATGTCGCTAGACACGCTGAGAACAGTTCTCCCTGAGGCTGAAC 243
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 Db 196 AGGAGTCCAAATCATGTCAATTTGACACGCTGCGAAATCAGTTCTCCCTGAGGCTGACC 255
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 QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTTAGATGGCTACACTTTG 303
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 Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTCTGTGCGGCTAGATGGGTACAGTTTG 315
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 QY 304 GACATCTGGGCGCCAGGAAACCTGTGTACCGTCTCCTCA 342
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 Db 316 GACTACTGGGCGCGGAAACCTGTGTACCGTCTCCTCA 354
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RESULT 5

HST22X1
 LOCUS H.sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone T22.1). 411 bp mRNA linear PRI 30-APR-1997

ACCESSION Z75385
 VERSION Z75385.1 GI:2062048
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 411); Tonnelie,C., D'Arcole,C., Depraetere,V., Metras,D., Boubli,D. and Fougereau,M.
 AUTHORS Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?

JOURNAL Int. Immunol. 9 (3), 407-414 (1997)

MEDLINE 97244170

REFERENCE 2 (bases 1 to 411)

PUBMED 9088979

AUTHORS Tonnelie,C.

TITLE Direct Submission

JOURNAL Submitted (26-JUN-1996) Cecile Tonnelie, Centre d'Immunologie

Marseille Luminy, Marseille, 13288, France

FEATURES Location/Qualifiers

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/organism="Homo sapiens"

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/db_xref="taxon:9606"

/chromosome="14"

/clone="T22.1"

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/tissue_type="thymus"

/clone_lib="T22"

/dev_stage="infant"

1..411

/product="Ig heavy chain variable region (VH4DJ)"

1..57

/sig_peptide

V_region 58..354

/note="Ig VH4-segment"

D_segment 355..377

J_segment 378..411

ORIGIN

Query Match 81.1%; Score 277.2; DB 9; Length 411;
 Best Local Similarity 88.8%; Pred. No. 6e-67;
 Matches 300; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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 Db 73 GAGTGGGCCCCAGGACTGGTGAAGCCTTTCACAGAACCTGTCCCTCACCTGCAGTGTCT 132
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 QY 64 GCGGCTCCATCCGCGAGTGGTGTACTACTGGAGTTGGATCCGCGCAACACCCAGGGAAG 123
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 Db 133 GGTGGCTCCATCAGCAGTGGTGTACTACTGGAGTGGATCCGCGCAGCACCCAGGGAAG 192
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 QY 124 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAAACACTTACAAACCCCGTCCCTC 183
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 QY 184 AAGAGTCCAAATGGCATGTCGCTAGACACGCTGTGAGAAAGTTCTCCCTGAGGCTGAAC 243
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 Db 253 AAGAGTCCAGTTACCATATCAGTAGACACGCGCTAAGAACCAAGTTCTCCCTGAAGCTGAGC 312
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 QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 303
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 Db 313 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTGGGTTATTGTAGTAGT 372
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 QY 304 GACATCTGGGCGCCAGGAAACCTGTGTACCGTCTCCTC 341
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 Db 373 TCCAGCTGGGCGCCAGGAAACCTGTGTACCGTCTCCTC 410
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RESULT 6

HSA491912
 LOCUS HSA491912
 DEFINITION Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region (clone HD17 C37).

ACCESSION AJ491912

VERSION AJ491912.1 GI:24415810

KEYWORDS constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Coker,H.A., Durham,S.R. and Gould,H.J.

AUTHORS Local somatic hypermutation and class switch recombination in the

TITLE nasal mucosa of allergic rhinitis patients

JOURNAL J. Immunol. 171 (10), 5602-5610 (2003)

MEDLINE 22970235

REFERENCE 2 (bases 1 to 432)

PUBMED 14607969

AUTHORS Coker,H.A.

TITLE Direct Submission

JOURNAL Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall

Centre, King's College London, Guy's Campus, London, SE1 1UL,

UNITED KINGDOM

FEATURES Location/Qualifiers

1..432

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/mol_type="mRNA"

/isolation_source="nasal biopsy from inferior turbinate of

allergic rhinitis patient"

/db_xref="taxon:9606"

/clone="HD17 C37"

/sex="female"

/cell_type="B lymphocyte"

/tissue_type="nasal mucosa"

/dev_stage="adult"

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/country="United Kingdom"

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/gene="IGHV4-30"

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/db_xref="GI:24415811"
/db_xref="REMTREMBL:CAD38015"
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/gene="IGHV4-30"
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356..432
/gene="IGH"
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356..432
/gene="IGH"
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region"

ORIGIN
Query Match 80.9%; Score 276.6; DB 9; Length 432;
Best Local Similarity 88.5%; Pred. No. 8.9e-67;
Matches 300; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 4 GAGCTGGCCAGGACTGGTGAAGCCCTGCAGACACCTGTCCTCAGCTCGCTGTCT 63
DB 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGAACCTGTCCTCAGCTGTCT 75
QY 64 GCGGCTCCATCCGAGTGGTGGTACTACTGAGTTGGATCGCCACACCCAGGAAG 123
DB 76 GGTGGGCCCATCAATAGTGGTGGTACTACTGAGCTGGATCGCCAGACCCAGGAAG 135
QY 124 GGCTGAGTGGATGGGTACATCTATCACAGTGGGAACACCTACAAACACCCGTCCTC 183
DB 136 GGCTGAGTGGATGGATGATCACTATACAGGGGAGCACCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATGCCATGTCGGTAGACACGTCTGAGAACAAAGTTCTCCCTGAGCTGAAC 243
DB 196 AGGAGTCGAATAATCATGTCAATGACACGTCTGCAATCAGTTCTCCCTGAGGCTGAAC 255
QY 244 TCTGTGACTCCCGGACACAGCGCGTGTATCTGTGCGAGGTAGATGGCTACATTTG 303
DB 256 TCTGTGACTCCCGGACACAGCGCGTGTATTTCTGTGCGGTCTAGATGGGTACAGTTG 315
QY 304 GACATCTGGGCCAGGAACCCCTGGTCACCGTCTCCCTCA 342
DB 316 GACTACTGGGCCAGGAACCCCTGGTCACCGTCTCCCTCA 354

RESULT 7
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LOCUS
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable
region, partial, clone 1-A34.
ACCESSION AJ244930
VERSION AJ244930.1 GI:4995319
KEYWORDS IGM; Igm heavy chain; immunoglobulin mu heavy chain; variable
region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

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AUTHORS
Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
Chiorazzi, N. and Ferrarini, M.
Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
marginal zone equivalents
J. Immunol. 164 (11), 5596-5604 (2000)
20281644
PUBMED 10820234
2 (bases 1 to 351)
Dono, M.
Direct Submission
Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
ITALY
FEATURES
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Best Local Similarity 90.1%; Pred. No. 1e-66;
Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 4 GAGCTGGCCAGGACTGGTGAAGCCCTGCAGACACCTGTCCTCAGCTCGCTGTCT 63
DB 10 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCTCAGCTGTCT 69
QY 64 GCGGCTCCATCCGAGTGGTGGTACTACTGAGTTGGATCGCCACACCCAGGAAG 123
DB 70 GGTGGCTCCATCAGAGTGGTGGTACTACTGAGCTGGATCGCCAGCACCCAGGAAG 129
QY 124 GGCTGAGTGGATGGGTACATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 183
DB 130 GGCTGAGTGGATGGGTACATCTATCACAGTGGGAGCACCTACTACAAACCCGTCCTC 189
QY 184 AAGAGTCGAATGCCATGTCGGTAGACACGTCTGAGAACAAAGTTCTCCCTGAGCTGAAC 243
DB 190 AAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGC 249
QY 244 TCTGTGACTCCCGGACACAGCGCGTGTATTACTGTGCGA---GGTTAGATGCTACACT 300
DB 250 TCTGTGACTCCCGGACACAGCGCGTGTATTACTGTGCGAGAGGCAAGAGGACTTCTAC 309
QY 301 TTGGACATCTGGGCCAGGAACCCCTGGTCACCGTCTCCCTCA 342
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RESULT 8
AX061463 360 bp DNA linear PAT 22-JAN-2001
LOCUS
DEFINITION Sequence 32 from Patent WO0100678.

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possible role in the control of tolerance in situ?

JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 414)
Tonnelle,C.
Direct Submission
TITLE
JOURNAL
Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie
Marseille Luminy, Marseille, 13288, France
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1. .57
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Matches 306; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
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Db 73 GAGTCTGCCAGACTGGTGAAGCTGCACAGACCCCTGTCCTCAGCTGCCTCTCTCT 132
Qy 64 GCGGCTCCATCCGAGTGGTGGTACTACTGGAGTGGATCGGCAACACCCAGGGAAG 123
Db 133 GGTGGCTCCATCAGCAGTGGTGGTACTACTGGAGTGGATCGGCAACACCCAGGGAAG 192
Qy 124 GGCCTGGAGTGGATGGTGGTACTATCAGAGTGGAGACCTACCAACCCGTCCTC 183
Db 193 GGCCTGGAGTGGATGGTGGTACTATCAGTGGAGACCTACCAACCCGTCCTC 252
Qy 184 AAGAGTGGATGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 243
Db 253 AAGAGTGGATGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 312
Qy 244 TCTGTGACTCGCGGACACCGCCGCTGTTACTGTGGAGGTTA---GATGGCTACACT 300
Db 313 TCTGTGACTCGCGGACACCGCCGCTGTTACTGTGGAGGTTA---GATGGCTACACT 372
Qy 301 TTGGACATCTGGGCGCAGGGAACCCCTGTCACCGTCTCCTC 341
Db 373 TTTGACTCTGGGCGCAGGGAACCCCTGTCACCGTCTCCTC 413

RESULT 11
HST14X4
LOCUS
DEFINITION H.sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone T14.4).
ACCESSION Z75378
VERSION 275378.1 GI:2062042
KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 414)
Tonnelle,C., D'Ercole,C., Depierre,V., Metras,D., Boubli,L. and

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 414)
Tonnelle,C.
Direct Submission
TITLE
JOURNAL
Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie
Marseille Luminy, Marseille, 13288, France
FEATURES
Location/Qualifiers
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ORIGIN

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Best Local Similarity 89.7%; Pred. No. 5.4e-66;
Matches 306; Conservative 0; Mismatches 32; Indels 3; Gaps 1;
Qy 4 GAGTCTGCCAGACTGGTGAAGCTGCACAGACCCCTGTCCTCAGCTGCCTCTCTCT 63
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Db 133 GGTGGCTCCATCAGCAGTGGTGGTACTACTGGAGTGGATCGGCAACACCCAGGGAAG 192
Qy 124 GGCCTGGAGTGGATGGTGGTACTATCAGAGTGGAGACCTACCAACCCGTCCTC 183
Db 193 GGCCTGGAGTGGATGGTGGTACTATCAGTGGAGACCTACCAACCCGTCCTC 252
Qy 184 AAGAGTGGATGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 243
Db 253 AAGAGTGGATGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 312
Qy 244 TCTGTGACTCGCGGACACCGCCGCTGTTACTGTGGAGGTTA---GATGGCTACACT 300
Db 313 TCTGTGACTCGCGGACACCGCCGCTGTTACTGTGGAGGTTA---GATGGCTACACT 372
Qy 301 TTGGACATCTGGGCGCAGGGAACCCCTGTCACCGTCTCCTC 341
Db 373 TTTGACTCTGGGCGCAGGGAACCCCTGTCACCGTCTCCTC 413

RESULT 12
HSA244949
LOCUS
DEFINITION H.sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone 3-A5.
ACCESSION AJ244949
VERSION AJ244949.1 GI:4995357
KEYWORDS Igm; Igm heavy chain; immunoglobulin mu heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1
AUTHORS    Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A.,
           Chiorazzi, N. and Ferrarini, M.
TITLE      Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
           marginal zone equivalents
JOURNAL    J. Immunol. 164 (11), 5596-5604 (2000)
MEDLINE    20281644
PUBMED     10820234
REFERENCE 2 (bases 1 to 357)
AUTHORS    Dono, M.
TITLE      Direct Submission
JOURNAL    Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
           sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
           ITALY
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Matches 309; Conservative 0; Mismatches 30; Indels 9; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGTGAAGCTGCACAGACCTCTCCCTCAGCTGCCTGTCCT 63
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Db 70 GTGTCTCCATCAGCAGTGGTGTACTACTGGAGTTGGATCCGCCAGCACCCAGGGAAG 129

QY 124 GGCCTGGAGTGGTGTACTATCTACAGTGGGAACACCTACAAACCCGTCCTC 183
Db 130 GGCCTGGAGTGGTGTACTATCTATACAGTGGGAACACCTACTACAACCCGTCCTC 189

QY 184 AAGAGTCGAATTCGCATGTCGTAGACGTCCTGAGAACAGTCTCCCTGAGGCTGAC 243
Db 190 AAGAGTCGATTACCATATCAGTAGACGTCCTTAGAACAGTCTCCCTGAGCTGAGC 249

QY 244 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGGAGTTAGAT-----GGC 294
Db 250 TCTGTGACTGCCCGGACACGCGCGTGTATTACTGTGGAGAGTATATAGAAGTACCAGC 309

QY 295 TACACTTTGACATCTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 342
Db 310 GACTACTTTGACTCTGGGGCCAGGAAACCTGTGTCACCGTCTCTCA 357

RESULT 13
HSA245064
LOCUS      HSA245064      354 bp      mRNA      linear      PRI 02-JUN-1999

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DEFINITION Homo sapiens mRNA for immunoglobulin gamma heavy chain variable
region, partial, clone 2-D123.
ACCESSION  AJ245064
VERSION     AJ245064.1 GI:4995589
KEYWORDS    IGG; IGG heavy chain; immunoglobulin gamma heavy chain; variable
region.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Dono, M., Zupo, S., Chiorazzi, N. and Ferrarini, M.
TITLE      Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic
           marginal zone equivalents
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 354)
AUTHORS    Dono, M.
TITLE      Direct Submission
JOURNAL    Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca
           sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova,
           ITALY
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QY 124 GSCCTGGAGTGGTGTATCATCTATCAGTGGGAACACCTACAACACCCGTCCTC 183
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QY 244 TCTGTGACTGCCGGGACACGCGCGTGTATTACTGTGGAGTTAGATGGCTTACTTTG 303
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Qy 304 GACATCTGGGCGCCAGGGAACCGCTGGTACACCGTCTCTCTCA 342
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RESULT 14
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LOCUS Human immunoglobulin heavy chain variable region (V4-31) gene,
DEFINITION partial cds.
ACCESSION U80129
VERSION U80129.1 GI:1791100
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 360)
AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE 9030878
PUBMED 9030878
REFERENCE 2 (bases 1 to 360)
AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
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Query Match 79.5%; Score 271.8; DB 9; Length 360;
Best Local Similarity 89.0%; Pred. No. 2e-65;
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Db 76 GGTGGCTCCATCAGCAGTGGTGGTTTACTACTGGAGTTGGATCCGCGACACCCAGGGAAG 135

Qy 124 GGCTGGAGTGGATTGGGTATCATCTATCACAGTGGGAACACTACAAACCCGTCCTC 183
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Qy 184 AAGAGTCGAATTGCCATGTCCGTAGACACGCTCTGAGACAGATTCTCCCTGAGGCTGAC 243
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Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGTGGAG-----GTTAGATGGCTAC 297
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Qy 298 ACTTTGACATCTCTGGGCGCCAGGGAACCGCTGGTACCGCTCTCTCA 342
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DEFINITION partial cds.
ACCESSION U80130
VERSION U80130.1 GI:1791102
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 360)
AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.
TITLE Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
JOURNAL Clin. Exp. Immunol. 107 (2), 372-380 (1997)
MEDLINE 97182739
PUBMED 9030878
REFERENCE 2 (bases 1 to 360)
AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
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ORIGIN
Query Match 79.5%; Score 271.8; DB 9; Length 360;
Best Local Similarity 89.0%; Pred. No. 2e-65;
Matches 307; Conservative 0; Mismatches 32; Indels 6; Gaps 1;

Qy 4 GAGTCTGCCCGACGACTGGTGAAGCCTTCACAGACCCCTGTCCTCTCTCT 63
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Qy 64 GCGGCTCCATCCGACGAGTGGTGGTTTACTACTGGAGTTGGATCCGCGACACCCAGGGAAG 123

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 2005.71 Seconds

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5091.898 Million cell updates/sec

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Scoring table: IDENTITY_NUC

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Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: em_estm:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_esti:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	260.8	76.3	607	12	BM783015
3	256.6	75.0	677	12	BG686767
4	253	74.0	490	14	CD689564

5	250.8	73.3	643	9	AU134293	AU134293
6	247	72.2	369	10	AW404242	AW404242 UI-HF-BL0
7	246	71.9	509	10	AW406349	AW406349 UI-HF-BL0
8	245.8	71.9	582	10	AW401348	AW401348 UI-HF-BL0
9	244.6	71.5	1108	12	BM920469	BM920469 AGENCOURT
10	241.8	70.7	914	12	BG757054	BG757054 602710478
11	240	70.2	363	10	AW403420	AW403420 UI-HF-BK0
12	239.4	70.0	813	13	BQ710364	BQ710364 AGENCOURT
13	238.2	69.6	903	13	BQ706579	BQ706579 AGENCOURT
14	237.8	69.4	828	10	BF974568	BF974568 602243482
15	237.2	69.4	890	13	BX324929	BX324929 BX324929
16	237.2	69.4	977	13	BX396901	BX396901 BX396901
17	237.2	69.4	1201	13	BX336959	BX336959 BX336959
18	236.8	69.2	904	13	BQ710488	BQ710488 AGENCOURT
19	236.2	69.1	814	12	BG685325	BG685325 602637756
20	236.2	69.1	1050	9	AL552672	AL552672 AL552672
21	235.2	68.8	447	10	AW402200	AW402200 UI-HF-BK0
22	235.2	68.8	1019	13	BQ072420	BQ072420 AGENCOURT
23	235	68.7	474	10	AW408410	AW408410 UI-HF-BK0
24	234.8	68.7	596	12	BM817833	BM817833 K-EST0084
25	234.6	68.6	942	13	BQ706244	BQ706244 AGENCOURT
26	233.8	68.4	661	12	BG686421	BG686421 602638356
27	233.6	68.3	542	10	AW951834	AW951834 EST363904
28	233.4	68.2	725	12	BG431274	BG431274 602439844
29	233.4	68.2	915	13	BQ706358	BQ706358 AGENCOURT
30	233.4	68.2	959	13	BH999307	BH999307 AGENCOURT
31	233.2	68.2	856	13	BQ421299	BQ421299 AGENCOURT
32	233	68.1	435	10	BF871158	BF871158 MR1-ET014
33	233	68.1	924	12	BG758027	BG758027 602715076
34	232.6	68.0	368	10	AW403989	AW403989 UI-HF-BK0
35	232.2	67.9	357	12	BP432480	BP432480 BP432480
36	232.2	67.9	921	13	BQ710000	BQ710000 AGENCOURT
37	232.2	67.9	925	13	BQ710876	BQ710876 AGENCOURT
38	231.8	67.8	367	10	AW403544	AW403544 UI-HF-BK0
39	231.8	67.8	924	13	BQ708516	BQ708516 AGENCOURT
40	231.8	67.8	1201	13	BX417108	BX417108 BX417108
41	231.4	67.7	1201	13	BX380759	BX380759 BX380759
42	231.2	67.6	421	10	AW407630	AW407630 UI-HF-BWC
43	230.4	67.4	1195	13	BQ707644	BQ707644 AGENCOURT
44	230	67.3	658	13	BX505812	BX505812 DKF2P686D
45	230	67.3	987	13	BQ707970	BQ707970 AGENCOURT

ALIGNMENTS

RESULT 1	AU122174	832 bp	mrna	linear	EST 01-AUG-2002
LOCUS	AU122174	MAMMAL	Homo sapiens	cdna	clone MAMMAL001802 5', mRNA
DEFINITION	AU122174	sequence.			
ACCESSION	AU122174				
VERSION	AU122174.1	GI:10937409			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 832)				
AUTHORS	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.				
TITLE	HRI human cDNA project				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of				

Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES
source

Location/Qualifiers
1..832
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MAMMA1001802"
/tissue_type="mammary gland"
/clone_lib="MAMMAL"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 79.0%; Score 270.2; DB 9; Length 832;
Best Local Similarity 87.3%; Pred. No. 2.5e-61;
Matches 296; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCGAGGACTGGTGAAGCTGACAGACCCCTGTCCTCAGCTGGCTGTCTCT 63
Db 110 GAGTGGGGCCGAGGACTGGTGAAGCTTTCACAGACCCCTGTCCTCAGCTGTCTCT 169

Qy 64 GCGGCTCCATCCGAGTGGTGGTTACTTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 170 GGTGGCTCCATCAGCAGTGGTGGAGCCCTACTGGAGTTGGATCCGCCAACCCAGGGAAG 229

Qy 124 GGCCTGGAGTGGTGGTACATCTATCACAGTGGGAACCTCAACAACCCCTGCCCTC 183
Db 230 GGCCTGGAGTGGTGGTACATCTATCAATGGGAACACTACTACAACCCCTGCCCTC 289

Qy 184 AAGAGTCGAATTGGCATGTGGTGAACAGCTGTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 290 AAGAGTCGAGTTACCATATCAACAGACATGTCGAAGACGAGTTCTCCCTGAAGCTAAAC 349

Qy 244 TCTGTGACTGCGGGACACCGCGGTGTTACTGTGGAGGTAGATGGCTACACTTTG 303
Db 350 TCTGTGACTGCGGGACACCGCGGTGTTACTGTGGAGGTAGATGGCTACACTTTG 409

Qy 304 GACATCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCA 342
Db 410 GACTTCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCA 448

RESULT 2
BM783015 607 bp mRNA linear EST 05-MAR-2002
LOCUS K-BST0060735 S18N669761 Homo sapiens cDNA clone S18N669761-2-E06
DEFINITION 5', mRNA sequence.

ACCESSION
BM783015
VERSION
BM783015.1 GI:19131247
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.

TITLE
21C Frontier Korean EST Project 2001
JOURNAL
Unpublished (2002)
COMMENT
Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: E column: 06
High quality sequence stop: 607.
Location/Qualifiers
1..607
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source

/db_xref="taxon:9606"
/clone="S18N669761-2-E06"
/sex="np"
/lab_host="Top10P"
/clone_lib="S18N669761"
/notes="Organ: Stomach; Vector: pcNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 76.3%; Score 260.8; DB 12; Length 607;
Best Local Similarity 86.8%; Pred. No. 6.7e-59;
Matches 302; Conservative 0; Mismatches 37; Indels 9; Gaps 1;

Qy 4 GAGTCTGGCCGAGGACTGGTGAAGCTGACAGACCCCTGTCCTCAGCTGGCTGTCTCT 63
Db 112 GAGTGGGGCCGAGGACTGGTGAAGCTTTCACAGACCCCTGTCCTCAGCTGTCTCT 171

Qy 64 GCGGCTCCATCCGAGTGGTGGTTACTTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 172 GGTGGCTCCATGACAGTGGTGGTTACTTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 231

Qy 124 GGCCTGGAGTGGTGGTACATCTATCAAGTGGGAACACTTACAAACCCCTGCCCTC 183
Db 232 GGCCTGGAGTGGTGGTACATCTATCACACTGGGAGCACTACTACAACCCCTGCCCTC 291

Qy 184 AAGAGTCGAATTGGCATGTGGTGAACAGCTGTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 292 AAGAGTCGAGTTACCATATCAACAGACATGTCGAAGACGAGTTCTCCCTGAAGCTGAGC 351

Qy 244 TCTGTGACTGCGGGACACCGCGGTGTTACTTACTGTGGAG-----GTAGATGGC 294
Db 352 TCTGTGACTGCGGGACACCGCGGTGTTACTTACTGTGGAGATGGCAATACGATATT 411

Qy 295 TACACTTTGGACATCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 412 TACGGTATGGACGTCTGGGGCCAAAGGGACCAACCGGTCAACCGTCTCTCTCA 459

RESULT 3
BG686767 677 bp mRNA linear EST 01-MAY-2001
LOCUS 602650737F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763217 5',
DEFINITION mRNA sequence.

ACCESSION
BG686767
VERSION
BG686767.1 GI:13918164
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 677)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLCM1618 row: i column: 10
 High quality sequence stop: 675.
 Location/Qualifiers
 1. .677
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4763217"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 75.0%; Score 256.6; DB 12; Length 677;
 Best Local Similarity 88.1%; Pred. No. 9.5e-58;
 Matches 304; Conservative 0; Mismatches 34; Indels 7; Gaps 2;
 QY 4 GAGTCGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTGCGCTGCTCT 63
 Db 99 GAGTCGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTGCGCTGCTCT 158
 QY 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTGGATCGGCAACCCAGGGAAG 123
 Db 159 GGTGGCTCCATCAGCAGTGGTGTACTACTGGAGTGGATCGGCAACCCAGGGAAG 217
 QY 124 GGCCTGGATGGATTGGGTACATCTATCAGTGGGAACACCTACACACCCGTCCTC 183
 Db 218 GGCCTGGATGGATTGGGTACATCTATCAGTGGGAACACCTACACACCCGTCCTC 277
 QY 184 AAGAGTCGAATTCGCAATCGGTAGACAGCTCTGAGAACAGTTCTCCCTGAGGCTGAAC 243
 Db 278 AAGAGTCGAATTCGCAATTCGGTAGACAGCTCTGAGAACAGTTCTCCCTGAGCTGAGC 337
 QY 244 TCTGTGACTGCGCGACACGCGCGGTGTTACTGTGCGA-----GGTGTAGTGGCTAC 297
 Db 338 TCTGTGACTGCGCGACACGCGCGGTGTTACTGTGCGAGAGATCGCAAGAGGAGGC 397
 QY 298 ACTTTGGACATCTGGGCGCAGGAACCCCTGTCACCGTCTCTCTCA 342
 Db 398 GGTTTCGACCCCTGGGCGCAGGAACCCCTGGTCAACCGTCTCTCTCA 442

RESULT 4
 CD689564
 LOCUS
 DEFINITION
 EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.
 CD689564
 VERSION
 CD689564.1 GI:32209443
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 490)
 AUTHORS
 Liu X.-O., Zhou Y., Zhang L.-J., Xu H., Chen H.-K., Pan Z.-G. and Zeng Y.-X.
 TITLE
 Transcriptional Gene Expression Profile of Human Nasopharynx
 JOURNAL
 Unpublished (2003)
 COMMENT
 Contact: Yixin Zeng
 Cancer Center

Sun Yat-sen University
 651 DongFeng Road East, Guangzhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn.

FEATURES

source

1. .490
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="normal nasopharynx"
 /clone_lib="human nasopharynx"
 /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 74.0%; Score 253; DB 14; Length 490;
 Best Local Similarity 85.9%; Pred. No. 7.2e-57;
 Matches 293; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
 QY 5 AGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTGAGCTGGGTGCTCTG 64
 Db 111 AGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTGAGCTGCTCTG 170
 QY 65 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTGGATCCGCCAACCCAGGGAAG 124
 Db 171 GTGACTCCATCAGCAGTGGTGTACTACTGGAGTGGATCCGCCAACCCAGGGAAG 230
 QY 125 GCGTGGAGTGGATTGGGTACATCTATCAGTGGGAACACCTACACAAACCCGTCCTCA 184
 Db 231 GCGTGGAGTGGATTGGGTACATCTATCAGTGGGAAGTCCGACTACACCCGTCCTCA 290
 QY 185 AGAGTCGAATTCGCAATCGGTAGACAGCTCTGAGAACAGTTCTCCCTGAGGCTGAAC 244
 Db 291 AGAGTCGAATTCGCAATTCGAGTACAGCTCTAAGAACCAAGTTCTCCCTGAGGTT 350
 QY 245 CTGTGACTCGCGGACACGCGCGGTGTTACTGTGCGAGGTTAGAT---GGCTACACTT 301
 Db 351 CTGTGAGCGCGGACACGCGCGGTATATTACTGTGCGAGATGGGTCCGCGAGATTAA 410
 QY 302 TGGACATCTGGGCGCAGGGAACCCCTGCTCACCGTCTCTCTCA 342
 Db 411 TTGACTACTGGGCGCAGGGAATCCTTGTCACCGTCTCTCTCA 451

RESULT 5
 AU134293
 LOCUS
 DEFINITION
 AU134293 OVARC1 Homo sapiens cDNA clone OVARC1001672 5', mRNA sequence.
 AU134293
 VERSION
 AU134293.1 GI:10994832
 EST.
 KEYWORDS
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 643)
 AUTHORS
 Ota T., Nishikawa T., Suzuki Y., Ishii S., Saito K., Kawai Y., Yamamoto J., Wakamatsu A., Nakamura Y., Nagai T., Sugano S. and Isogai T.
 TITLE
 HRI human cDNA project
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5' & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and

FEATURES
source
1. .643
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="OVARC1001672"
/tissue_type="ovary, tumor tissue"
/clone_lib="OVARC1"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 73.3%; Score 250.8; DB 9; Length 643;
Best Local Similarity 84.6%; Pred. No. 3.3e-56;
Matches 301; Conservative 0; Mismatches 37; Indels 18; Gaps 1;
QY 5 AGTCTGGCCAGGACTGGTGAAGCTGCACAGACCTGCTCCCTAGCTGCGCTGTCTCTG 64
Db 110 AGTCGGGCCAGGACTGGTGAAGCTTCACAGACCTGCTCCCTACCTGCACTGTCTCTG 169
QY 65 GCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAGG 124
Db 170 GTGACTCCATCAGCAGTGGTGAATTAATCTGGAACCTGGATCCGCCAACACCCAGGGAAGG 229
QY 125 GCCTGGAGTGAATGGGTACATATATACAGTGGGAACACCTAACAACCCGTCCTCA 184
Db 230 GCCTTGAAGTGGGTACATATATACAGTGGGAACACCTAACAACCCGTCCTCA 289
QY 185 AGAGTCGATTTGCCATGTCGGTAGACAGCTCTGAGAACAGTTCTCCCTGAGGCTGAAT 244
Db 290 AGAGTCGAGTTACCATATCAATAGACAGCTCTAAGAACCCGTTCTCCCTGAGGCTGAAGC 349
QY 245 CTGTGACTGCGCGGACACGCGGTGTTACTGTGGAGGTTAGATGGCTACACT--- 300
Db 350 CTGTGACTGCGCGGACACGCGGTGTTACTGTGGAGGTTAGATGGCTACACT--- 409
QY 301 -----TTGACATCTGGGCCAGGGAACCTCGTCAACCGTCTCCTCA 342
Db 410 GGACCTACAGTAAGTTTGACCACTGGGGCCAGGGAACCTCGTCAACCGTCTCCTCA 465

RESULT 6
AW404242 369 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BL0-abg-f-09-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3057545 5', mRNA sequence.
ACCESSION AW404242
VERSION AW404242.1 GI:6923299
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source
1. .369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source
1. .643
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OVARC1001672"
/tissue_type="ovary, tumor tissue"
/clone_lib="OVARC1"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 72.2%; Score 247; DB 10; Length 369;
Best Local Similarity 85.9%; Pred. No. 2.5e-55;
Matches 274; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCTGCTCCCTAGCTGCGCTGTCTCT 63
Db 34 GAGTCGGGCCAGGACTGGTGAAGCTTCACAGACCTGCTCCCTACCTGCACTGTCTCT 93
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 94 GGTGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCCAACACCCAGGGAAG 153
QY 124 GGCCTGGAGTGGATGGGTACATCTATCAGAGTGGGAACACCTACAAACCCGTCCTC 183
Db 154 GGCCTGGAGTGGATGGGTACATCTATCAGAGTGGGAACACCTACAAACCCGTCCTC 213
QY 184 AAGAGTCGAATGGCCATGTCGGTAGACAGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 214 AAGAGTCGGCTTACCATGTCAATAGACACGCTCTAAGAACCAAGTTCTCCCTGAAACTGAGC 273
QY 244 TCTGTGACTGCGCGGACACGCGGTGTTACTGTGGAGTGGATGGCTAGATGGCTACACTTTG 303
Db 274 TCTGTGACTGCGCGGACACGCGGTGTTACTGTGGAGTGGATGGCTAGATGGCTACACTTTG 333
QY 304 GACATCTGGGCCAGGGA 322
Db 334 GATAGTAGTGGTTACGGAA 352

RESULT 7
AW406349 509 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BL0-aco-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3059933 5', mRNA sequence.
ACCESSION AW406349
VERSION AW406349.1 GI:6925406
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 509)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

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source
1. .509
/organism="Homo sapiens"
/mol_type="mRNA"

/clone="IMAGE:3057545"
/tissue_type="lymph"
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/cell_line="MGC85"
/lab_host="DR10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 72.2%; Score 247; DB 10; Length 369;
Best Local Similarity 85.9%; Pred. No. 2.5e-55;
Matches 274; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCTGCTCCCTAGCTGCGCTGTCTCT 63
Db 34 GAGTCGGGCCAGGACTGGTGAAGCTTCACAGACCTGCTCCCTACCTGCACTGTCTCT 93
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 94 GGTGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCCAACACCCAGGGAAG 153
QY 124 GGCCTGGAGTGGATGGGTACATCTATCAGAGTGGGAACACCTACAAACCCGTCCTC 183
Db 154 GGCCTGGAGTGGATGGGTACATCTATCAGAGTGGGAACACCTACAAACCCGTCCTC 213
QY 184 AAGAGTCGAATGGCCATGTCGGTAGACAGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 214 AAGAGTCGGCTTACCATGTCAATAGACACGCTCTAAGAACCAAGTTCTCCCTGAAACTGAGC 273
QY 244 TCTGTGACTGCGCGGACACGCGGTGTTACTGTGGAGTGGATGGCTAGATGGCTACACTTTG 303
Db 274 TCTGTGACTGCGCGGACACGCGGTGTTACTGTGGAGTGGATGGCTAGATGGCTACACTTTG 333
QY 304 GACATCTGGGCCAGGGA 322
Db 334 GATAGTAGTGGTTACGGAA 352

RESULT 7
AW406349 509 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BL0-aco-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3059933 5', mRNA sequence.
ACCESSION AW406349
VERSION AW406349.1 GI:6925406
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 509)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
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/db_xref="taxon:9606"
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 /lab_host="DH10B (LTI)"
 /clone_lib="NIH_MGC 37"
 /note="Vector: pW73-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 71.9%; Score 246; DB 10; Length 509;
 Best Local Similarity 84.5%; Pred. No. 5.5e-55;
 Matches 289; Conservative 0; Mismatches 50; Indels 3; Gaps 1;
 QY 4 GAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
 DB 54 GAGTCGGGCCAGGACTGGTGAAGCTTCGGAGACCTGTCCCTACCTGCACATGTCTCT 113
 QY 64 GCGGCTCCATCCGACGTGGTGGTACTACTGAGTGGATCCGCCAACACCCAGGGAAG 123
 DB 114 GGTGGCTCCATCAGCAGTAGTAGTACTACTGGGGCTGGATCCGCCAGCCCAAGGAAG 173
 QY 124 GGCTGGAGTGGATGGGTACATCATCAGTGGGAAACACCTACACACCCGTCCCTC 183
 DB 174 GGGCTGAGTGGATGGGAGTATCTATTATAGTGGGAGCACCTACTACACCCGTCCCTC 233
 QY 184 AAGAGTGGAAATGGCATGTGGTACACAGCTCTCAGAACAGTTCCTCCGTGAGCTGAAC 243
 DB 234 AAGAGTGGATCCACCATATCAGTAGACAGCTCCAGAACCGATTCCTCGAAGCTGAGC 293
 QY 244 TCTGTACTCCGCGGACACGGCGTGTATTACTGTGCGAG---GTTAGATGGCTACACT 300
 DB 294 TCTGTAGCCCGCGGACACGGCGTGTATTACTGTGCGAGACCTCTCTACGAGCCTGG 353
 QY 301 TTGGACATCTGGGCGCAGGAACCTGTACCGTCTCTCTCA 342
 DB 354 TTGACCCCTGGGCGCAGGAACCTGTACCGTCTCTCTCA 395

RESULT 8
 AW401348
 LOCUS
 DEFINITION UI-HF-BKO-aau-d-08-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
 IMAGE:3055142 5', mRNA sequence.
 AW401348
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 582)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Unpublished (1999)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.

FEATURES
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/mol_type="mRNA"
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 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH_MGC 36"
 /note="Vector: pW73-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 71.9%; Score 245.8; DB 10; Length 582;
 Best Local Similarity 86.1%; Pred. No. 6.7e-55;
 Matches 297; Conservative 0; Mismatches 42; Indels 6; Gaps 2;
 QY 4 GAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
 DB 34 GAGTCGGGCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCTCAGTGGCTGTCTCT 93
 QY 64 GCGGCTCCAT---CGCAGTGGTGGTACTACTGAGTGGATCCGCCAACACCCAGGG 120
 DB 94 GGTGGCTCCATCTCTCAACAGTGGTATTCTCTGGACTTGGATCCGCCAGACCCAGGG 153
 QY 121 AAGGCGCTGGAGTGGATGGGTACATCTATCAGTGGGAAACACCTACACACCCGTCC 180
 DB 154 AAGGCGCTGGAGTGGATGGTACCTATTACACTGGGAGACCTATTACACCCGTCC 213
 QY 181 CTCAAGAGTGGATGGCATGTGGTAGACAGCTCTGAGAACAGTTCCTCCGTGAGCTG 240
 DB 214 CTCAAGAGTGGATGGTTCATATCAGTGGACACGCTCTAAGAACAGTTCCTCCGTGAGCTG 273
 QY 241 AACTCTGTGACTCCGCGGACACGGCGTGTATTACTGTGCGAGGTAGATGGCTAC--- 297
 DB 274 AGCTCTGACTCCGCGGACACGGCCATGTATTACTGTGCGAGAGGGTGCCTACTAT 333
 QY 298 ACTTTGGACATCTGGGCGCAGGAACCCCTGGTACCGCTCTCTCTCA 342
 DB 334 GC'TTTGATATCTGGGCGCAGGAACATGTCACCGTCTCTCTCA 378

RESULT 9
 BM920469
 LOCUS
 DEFINITION BM920469 1108 bp mRNA linear EST 12-MAR-2002
 AGENCOURT 6709612 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750444
 5', mRNA sequence.
 BM920469
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 1108)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Unpublished (1999)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12781 row: g column: 21
 High quality sequence stop: 626.
 Location/Qualifiers
 1. .1108

FEATURES
 source
 1. .1108

/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5750444"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match 71.5%; Score 244.6; DB 12; Length 1108;
Best Local Similarity 84.1%; Pred. No. 2e-54;
Matches 290; Conservative 0; Mismatches 49; Indels 6; Gaps 1;
QY 4 GAGTCTGCCAGGACTGGTGAAGCTGCACAGACCCCTGCTCCCTCAGCTGGCTGTCTCT 63
Db 110 GAGTGGGGCCAGGACTGGTGAAGCTTTCGGAGACCCCTGCTCCCTCAGCTGTCTCT 169
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTTACTTGGAGTGGATCCGCGCAACACCCAGGGAAG 123
Db 170 GGTGCTCCGTCAGCAGTGGTGGTTACTTACTTGGAGTGGATCCGCGAGCCGCCAGGGAAG 229
QY 124 GGCCTGGAGTGGTGGTGGTACATCATCAGTGGGAACACCTACAAACCCGCTCCCTC 183
Db 230 GGACTGGAGTGGTGGTGGTATATCTATTAGAGTGGAGCACCACCACTACAAACCCCTCCCTC 289
QY 184 AAGAGTGAATTGGCATGTGGTAGACAGCTGTGAGACAGTTCCTCCCTGAGGCTGAAC 243
Db 290 AAGAGTGCAGTCCACATATCAGTAGACACGTCCTCAAGAACCAAGTTCCTCCCTGAGCTGAGC 349
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGA-----GGTAGATGGCTAC 297
Db 350 TCTGTGACCGCTGCGGACACGCGCTGTATTACTGTGGAAGCGCGGGGGGGGGGAGCTAC 409
QY 298 ACTTTGGACATCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 410 TACATGGAGCTCTGGGGCAAGGGACCAAGGTCACCGTCTCTCTCA 454

RESULT 10
BG757054 914 bp mRNA linear EST 15-MAY-2001
LOCUS 602710478F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850851 5',
DEFINITION mRNA sequence.
ACCESSION BG757054
VERSION BG757054.1 GI:14067707
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 914)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
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High quality sequence stop: 854.
Location/Qualifiers
1. .914
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:4850851"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.9kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 70.7%; Score 241.8; DB 12; Length 914;
Best Local Similarity 85.3%; Pred. No. 1e-53;
Matches 296; Conservative 0; Mismatches 42; Indels 9; Gaps 2;
QY 4 GAGTCTGCCAGGACTGGTGAAGCTGCACAGACCCCTGCTCCCTCAGCTGGCTGTCTCT 63
Db 93 GAGTGGGGCCAGGACTGGTGAAGCTTTCACAGACCCCTGCGCCTCAGCTGTCTCT 152
QY 64 GCGGCTCCATCCGAGTGGTGGTTACTTACTTGGAGTGGATCCGCGCAACACCCAGGGAAG 123
Db 153 GGTGCTCCATCAGCAGTGGTGGTTACTTACTTGGAGTGGATCCGCGAGCAGCCCA-GGAAG 211
QY 124 GGCCTGGAGTGGTGGTGGTACATCATCAGTGGGAACACCTACAAACCCGCTCCCTC 183
Db 212 GGCCTGGAGTGGTGGGAACATCTATACAGTGGGAGCAGCTACTACATCCGCTCCCTC 271
QY 184 AAGAGTGAATTGGCATGTGGTAGACACGCTGTGAGAAACAAGTTCCTCCCTGAGGCTGAAC 243
Db 272 AAGAGTGCAGTTCACATATCAGTAGACACGCTTAAGAACCAAGTTCCTCCCTGAGCTGAGC 331
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTTGTGGAGGTAGAGTGGCTACACTTTG 303
Db 332 TCTGTGACTGCGCGGACACGCGCTGTATTATTGTGCGAGAGGGAAGACTACCGTGGC 391
QY 304 GACATCT-----GGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 392 CACGACTTTGACTACTGGGGCCAGGAACCCCTGGTCAACCGTCTCTCTCA 438

RESULT 11
AW403420 363 bp mRNA linear EST 16-FEB-2000
LOCUS UI-HF-BKO-abe-g-03-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3056068 5', mRNA sequence.
ACCESSION AW403420
VERSION AW403420.1 GI:6922356
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 363)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/brp/image/image.html
Seq primer: M13 Forward.

FEATURES

source
Location/Qualifiers

1. .363
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/cell_line="MGC85"
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/clone_lib="NIH_MGC 36"
/notes="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 70.2%; Score 240; DB 10; Length 363;
Best Local Similarity 90.7%; Pred. No. 1.8e-53;
Matches 255; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCCTGCACAGACCTGTCCCTCAGCTGGCTGTCTCT 63
|||
Db 34 GAGTCGGGGCCAGGACCGTGAAGCCCTTCACAGACCTGTCCCTCAGCTGTCTCT 93
|||
QY 64 GCGGGCTCCATCCGACGTGTGGTTACTTACTGGAGTTGGATCGCCAAACCCAGGGAAG 123
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Db 94 GGTGGCTCCATCAGCAGTGTGGTTACTTACTGGACCTGGATCGCCAGCAGCGANGAAG 153
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QY 124 GGCTGGAGTGGATGGGTACATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 183
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Db 154 GGCTGGAGTGGATGGGTACATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 213
|||
QY 184 AAGAGTCGAATTGCCATTCGTTAGACACGTCTGAGAACAGTTCTCCCTGAGGCTGAAC 243
|||
Db 214 AAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACAGTTCTCCCTGAAGCTGAAC 273
|||
QY 244 TCTGTGACTCCGGGACACGGCGGTGTATTACTTGTGCGGAG 284
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Db 274 TCTGTGACTCCGGGACACGGCGGTGTATTACTTGTGAG 314
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RESULT 12

BQ710364

LOCUS BQ710364 813 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8351485 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282412
5', mRNA sequence.

ACCESSION

BQ710364

VERSION BQ710364.1 GI:21849263
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 813)

NIH-MGC <http://imgc.ncbi.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-@email.nih.gov

TITLE

Tissue Procurement: Dr. Mark Watson

JOURNAL

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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High quality sequence stop: 529.
Location/Qualifiers

1. .813
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/clone_lib="NIH_MGC 113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.0%; Score 239.4; DB 13; Length 813;
Best Local Similarity 90.7%; Pred. No. 4.1e-53;
Matches 255; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCCTGCACAGACCTGTCCCTCAGCTGGCTGTCTCT 63
|||
Db 82 GAGTCGGGGCCAGGACTGGTGAAGCCCTTCACAGACCTGTCCCTCAGCTGTCTCT 141
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QY 64 GCGGGCTCCATCCGACGTGTGGTTACTTACTGGAGTTGGATCGCCAAACCCAGGGAAG 123
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Db 142 GGTGGCTCCATCAGCAGTGTGGTTACTTACTGGAGCTGGATCGCCAGCAGCGGGAAG 201
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QY 124 GGCTGGAGTGGATGGGTACATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 183
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QY 184 AAGAGTCGAATTGCCATTCGTTAGACACGTCTGAGAACAGTTCTCCCTGAGGCTGAAC 243
|||
Db 262 AAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACAGTTCTCCCTGAAGATGAAC 321
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QY 244 TCTGTGACTCCGGGACACGGCGGTGTATTACTTGTGCGGAG 284
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Db 322 TCTGTGACTCCGGGACACGGCGGTGTATTACTTGTGCGGAG 362
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RESULT 13

BQ706579

LOCUS BQ706579 903 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8487944 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300935
5', mRNA sequence.

ACCESSION

BQ706579

VERSION BQ706579.1 GI:21845478
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 903)

NIH-MGC <http://imgc.ncbi.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-@email.nih.gov

TITLE

Tissue Procurement: Dr. Mark Watson

JOURNAL

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM2515 row: p column: 24
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High quality sequence stop: 584.
Location/Qualifiers

FEATURES
source

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CS0DI086YJ13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 59.4%; Score 237.2; DB 13; Length 890;
Best Local Similarity 82.2%; Pred. No. 1.7e-52;
Matches 291; Conservative 0; Mismatches 48; Indels 15; Gaps 1;
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Db |||||
QY 133 GAGTCGGGCCAGGACTGGTGAAGCCTTCGAGACCCCTGTCCCTCAGCTGTCTCT 192
Db |||||
QY 64 GCGGGTCCATCCGCACTGGTGGTTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db |||||
QY 193 GGTGGCTCCATCAGCACTAGTACTTACTTGGGGCTGGATCCGCCAGCCCCAGGGAAG 252
Db |||||
QY 124 GGCCTGGAGTGGATTGGGTACATCTATCAGTGGGAACCTACACAAACCCGTCCCTC 183
Db |||||
QY 253 GGGCTGGAGTGGATTGGGACTATCTATTATAGTGGAGACCTACTACAAACCCGTCCCTC 312
Db |||||
QY 184 AAGAGTCGAATTGCCATGTCGGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db |||||
QY 313 AAGATCGAGTCCACATATCAGTAGACACGTCAGAACCCAGTTCTCCCTGAGGCTGAGC 372
Db |||||
QY 244 TCTGTGACTCCCGGGACACGGCGGTGTATTACTGTCCGAGGTTAGATGG----- 293
Db |||||
QY 373 TCTGTGACCGCGGGACACGGCGGTGTATTACTGTCCGAGTGGTTGTAGTGGTATAGC 432
Db |||||
QY 294 -----CTACACTTTGGACATCTGGGGCCAGGGAACCCGTGTCACCGTCTCTCA 342
Db |||||
QY 433 TGCTACCTCGCCTTTGACTACTGGGGCCAGGGAACCCGTGTCACCGTCTCTCA 486
Db |||||

Search completed: August 13, 2004, 07:13:17
Job time : 2011.71 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 222.818 Seconds
(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725A-1
Perfect score: 342
Sequence: 1 ctgagctctggccaggact.....ccctgtaccgtctctca 342

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002s:.*
7: Geneseqn2003as:.*
8: Geneseqn2003bs:.*
9: Geneseqn2003cs:.*
10: Geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	340.4	99.5	342	6	ABK89637 DNA encod
2	308.4	90.2	342	6	ABK89639 DNA encod
3	297.2	86.9	342	6	ABK89638 DNA encod
4	276.4	80.8	360	4	Aaf29076 Human HIV
5	275	80.4	352	9	Adc99786 Anti-huma
6	275	80.4	352	9	Add05390 Anti-MUC1
7	265.8	77.7	369	4	Aaf29046 Human HIV
8	265.4	77.6	352	9	Adc99778 Anti-huma
9	265.4	77.6	352	9	Add05382 Anti-MUC1
10	265.2	77.5	358	9	Adc99798 Anti-huma
11	265.2	77.5	358	9	Add05402 Anti-MUC1
12	260.8	76.3	516	3	Aaa46876 DNA encod
13	256.4	75.0	352	9	Adc99806 Anti-huma
14	255.4	75.0	352	9	Add05410 Anti-MUC1
15	255.6	74.7	357	2	AaQ38670 MAB GAH v
16	254.4	74.4	366	4	Aaf29066 Human HIV
17	250.8	73.3	1644	2	Aaz22434 Human bla
18	250.2	73.2	741	3	Aaz28998 Anti-muri
19	249	72.8	324	4	Abs46332 Human liv
20	248.6	72.7	631	2	AaQ78969 Human imm
21	248.6	72.7	1567	4	Aac66522 Human imm
22	248.4	72.6	340	6	ABK84446 Human CDN
23	248.4	72.6	340	7	ACA64884 Human Ig

24	247.8	72.5	450	2	AAX90024 Human mon
25	246.2	72.0	467	7	ABZ59692 Anti-TRAI
26	245.8	71.9	381	6	ABK24406 Heavy cha
27	245.8	71.9	384	6	ABK24410 Heavy cha
28	244.2	71.4	381	6	ABK24408 Heavy cha
29	243	71.1	467	7	ABZ59694 Anti-TRAI
30	241	70.5	466	3	Aaz42292 Human 5'
31	241	70.5	1543	4	Aaf97947 Human sec
32	240.4	70.3	393	3	Aac98188 Human col
33	240	70.2	504	3	Aaz42341 Human 5'
34	239.2	69.9	378	3	AAC62336 DNA encod
35	236.8	69.2	614	2	AAV86218 EST clone
36	236.6	69.2	351	3	Aaz49608 DNA-1 rel
37	236.6	69.2	351	3	Aaz49590 Human ant
38	233.8	68.4	366	2	AAQ33035 MAB 1-3-1
39	233.6	68.3	462	7	ABT31873 Anti-CD40
40	233	68.1	357	4	AAS03405 DNA encod
41	232.6	68.0	360	5	AAF29506 Human Fab
42	232.4	68.0	372	4	AAF29051 Human HIV
43	229.6	67.1	417	3	Aaz39316 Nucleotid
44	228.6	66.8	471	7	ACD10940 Human epi
45	228.2	66.7	1212	2	AAQ78999 Human imm

ALIGNMENTS

RESULT 1
ABK89637
ID ABK89637 standard; DNA; 342 BP.
XX
AC ABK89637;
XX
DT 21-OCT-2002 (first entry)
XX
DE DNA encoding human IgE Fab clone 94 heavy chain.
XX
KW Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..342
FT /tag= a
FT /product= "Fab clone 94 heavy chain"
FT misc_feature 7..78
FT /tag= b
FT /note= "PR1 region"
FT misc_feature 79..99
FT /tag= c
FT /note= "CDR1 region"
FT misc_feature 100..123
FT /tag= d
FT /note= "PR2 region"
FT misc_feature 134..141
FT /tag= e
FT /note= "PR3 region"
FT misc_feature 142..189
FT /tag= f
FT /note= "CDR2 region"
FT misc_feature 190..285
FT /tag= g
FT /note= "PR3 region"
FT misc_feature 286..309
FT /tag= h
FT /note= "CDR3 region"
FT misc_feature 310..342
FT /tag= i
FT /note= "PR4 region"
PN WO200253595-A1.
XX

```
PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
XX
DR P-PSDB; ABG30445.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX Disclosure; Page 31-32; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for blocking the binding of grass pollen allergenic patients
CC IgE antibodies to Phi p 2. The present sequence represents the DNA
CC encoding the human IgG fab, clone 94 heavy chain protein of the invention
XX
SQ Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;

Query Match
Best Local Similarity 99.5%; Score 340.4; DB 6; Length 342;
Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGCCCTCAGCTGCCTGTC 60
Db |||||
1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGCCCTCAGCTGCCTGTC 60
QY 61 TCTGGCGGCTCCATCCGAGTGGTGGTTACTACTCGAGTTGGATCGGCCAACACCCAGGG 120
Db |||||
61 TCTGGCGGCTCCATCCGAGTGGTGGTTACTACTCGAGTTGGATCGGCCAACACCCAGGG 120
QY 121 AAGGGCCTGGAGTGGGTTACATCTATCAGTGGGACACCTACAAACCCGTC 180
Db |||||
121 AAGGGCCTGGAGTGGGTTACATCTATCAGTGGGACACCTACAAACCCGTC 180
QY 181 CTCAGAGTCAATTCGATGTCGTAGACACGTCGTAGAACAGTTCTCCCTGAGGCTG 240
Db |||||
181 CTCAGAGTCAATTCGATGTCGTAGACACGTCGTAGAACAGTTCTCCCTGAGGCTG 240
QY 241 AACTCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGTGGCTACT 300
Db |||||
241 AACTCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGTGGCTACT 300
QY 301 TTGGACATCTGGGGCCAGGGAACCTGGTCAACCGTCTCTCA 342
Db |||||
301 TTGGACATCTGGGGCCAGGGAACCTGGTCAACCGTCTCTCA 342

RESULT 2
ABK89639
ID ABK89639 standard; DNA; 342 BP.
XX
AC ABK89639;
XX
```

```
DT 21-OCT-2002 (first entry)
XX
DE DNA encoding human IgE Fab clone 100 heavy chain.
XX
KW Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 1..342
FT /product= "Fab clone 100 heavy chain"
FT /tag= a
FT misc_feature 7..78
FT /tag= b
FT /note= "FR1 region"
FT misc_feature 79..99
FT /tag= c
FT /note= "CDR1 region"
FT misc_feature 100..123
FT /tag= d
FT /note= "FR2 region"
FT misc_feature 134..141
FT /tag= e
FT /note= "FR3 region"
FT misc_feature 142..189
FT /tag= f
FT /note= "CDR2 region"
FT misc_feature 190..285
FT /tag= g
FT /note= "FR3 region"
FT misc_feature 286..309
FT /tag= h
FT /note= "CDR3 region"
FT misc_feature 310..342
FT /tag= i
FT /note= "FR4 region"
XX
XX WO200253595-A1.
XX
XX 11-JUL-2002.
PD
PF 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
PR
PR (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR P-PSDB; ABG30445.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX Disclosure; Page 33; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have anti-allergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergenic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for blocking the binding of grass pollen allergenic patients
CC may be used for blocking the binding of grass pollen allergic patients
```

CC	IgE antibodies to Phi p 2. The present sequence represents the DNA
CC	encoding the human IgG fab, clone 100 heavy chain protein of the
CC	invention
XX	
SQ	Sequence 342 BP; 69 A; 103 C; 94 G; 76 T; 0 U; 0 Other;
	Query Match 90.2%; Score 308.4; DB 6; Length 342;
	Best local Similarity 93.9%; Pred. No. 1.3e-78;
	Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY	1 CTGGAGTCTGGCCCGCAGGACTGGTGAAAGCCCTGCACAGACCCTGTCCCTCAGCTGCCTGTC 60
DB	1 CTGGAGTCTGGCCCGCAGGACTGGTGAAAGCCCTGCACAGACCCTGTCCCTCAGCTGCCTGTC 60
QY	61 TCTGGGGCTGCCATCCCAGTGGTGGTTACTTACTGGAGTTGGATCCGCCAACACCCAGGG 120
DB	61 TCTGGTGGCTCCATCCGAGTGGTGGTTATTACTTGGAGTTGGATCCGCCAGCTCCAGGG 120
QY	121 AAGGGCCTGGAGTGGATTGGGTACAATCATCATCAAGTGGGAACACTTACAACAACCCGTCC 180
DB	121 AAGGGCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACCTACTACAACCCGTCC 180
QY	181 CTCAAGAGTCCAATTGGCCATCTCGGTAGACACAGTCTGAGAACAGATTCTCCCTGAGGCTG 240
DB	181 CTCAAGAGTCCAGTTACCATGTCTAGTAGACACGCTTAAGAACCACCTTCTCCCTGAGGCTG 240
QY	241 AAATCTGTGACTGCCGGGACACAGCCGCTGTATTACTGTGCGAGGTTAGATGGCTACACT 300
DB	241 AGCTCTGTGACTGCCGGGACACAGCCGCTGTATTACTGTGCGAGGTCAGATGGCTACACT 300
QY	301 TTGGACATCTGGGGCCGAGGGAACCCCTGGTCAACCGTCTCCTCA 342
DB	301 TTGGACAACTGGGGCCAGGGAAACCCCTGGTCAACCGTCTCCTCA 342
RESULT 3	
ABK89638	
ID	ABK89638 standard; DNA; 342 BP.
XX	ABK89638;
XX	
DT	21-OCT-2002 (first entry)
DE	DNA encoding human IgE Fab clone 60 heavy chain.
KW	Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
KW	timothy grass pollen allergen; passive immunotherapy.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
CDS	1..342
FT	/tag= a
FT	/product= "Fab clone 60 heavy chain"
FT	misc_feature 7..78
FT	/tag= b
FT	/note= "FR1 region"
FT	misc_feature 79..99
FT	/tag= c
FT	/note= "CDR1 region"
FT	misc_feature 100..123
FT	/tag= d
FT	/note= "FR2 region"
FT	misc_feature 134..141
FT	/tag= e
FT	/note= "FR3 region"
FT	misc_feature 142..189
FT	/tag= f
FT	/note= "CDR2 region"
FT	misc_feature 190..285
FT	/tag= g
FT	/note= "FR3 region"
FT	misc feature 286..309

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RESULT 4
AAF29076
ID AAF29076 standard; DNA; 360 BP.
XX
AC AAF29076;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX envelope glycoprotein; gp120; diagnosis; ds.
XX
OS Homo sapiens.
XX
FN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US017327.
XX
PR 30-JUN-1999; 99US-0141701P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
DR P-PSDB; AAB62775.
XX
XX Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal.
XX
PS Claim 4; Page 45; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection
XX
SQ Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

Query Match      80.8%; Score 276.4; DB 4; Length 360;
Best Local Similarity 90.1%; Pred. No. 2e-69;
Matches 308; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

QY 4 GAGTCTGCCAGGACTGGTGAAGCCTGCACAGACCTGTCCCTCAGCTGGCGTGTCTCT 63
Db 19 GAGTGGGCCAGGACTGGTGAAGCCTGCACAGACCTGTCCCTCAGCTGTCTCTCT 78

QY 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTGGATCCGCAACACCCAGGGAAG 123
Db 79 GGTGGCTCCATCAGCAGTGGTGTACTACTGGAGTGGATCCGCAACACCCAGGGAAG 138

QY 124 GGCCTGGAGTGGTGTACATCTATCAGAGTGGGACACCTACACAAACCCGTCCTC 183
Db 139 GGCCTGGAGTGGTGTACATCTATTACAGTGGGACACCTACTACAAACCCGTCCTC 198

QY 184 AAGAGTCGAATGGCCATCTCGGTAGACACAGTCTCGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 199 AAGAGTCGAGTTACCATATCAGTAGACACAGTCTAAGAACACAGTTCTCCCTGAGGCTGAGC 258

QY 244 TCTGTGACTGGCGGACACGCGGTGTATTACTGTGGA---GGTTAGATGGCTACACT 300
Db 259 TCTGTGACTGGCGGACACGCGGTGTATTACTGTGCGAGAGGGGTAGTAGTGACTGG 318

QY 301 TTGACATCTGGGGCCAGGGAACCTGGTTCACCGTCTCTCTCA 342
Db 319 TTGACCCCTGGGGCCAGGGAACCTGGTTCACCGTCTCTCTCA 360
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RESULT 5
ADC99786
ID ADC99786 standard; DNA; 352 BP.
XX
AC ADC99786;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX cytotstatic; melanoma; oesophageal; pancreatic; colorectal tumour;
XX cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX lung cancer; human; ds; gene.
XX
OS Homo sapiens.
XX
FN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
DR WPI; 2003-587113/55.
DR P-PSDB; ADC99784.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 8; SEQ ID NO 15; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
XX
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match      80.4%; Score 275; DB 9; Length 352;
Best Local Similarity 90.3%; Pred. No. 5e-69;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCTGTCCCTCAGCTGGCGTGTCTCT 63
Db 16 GAGTGGGCCAGGACTGGTGAAGCCTGCACAGACCTGTCCCTCAGCTGTCTCTCT 75

QY 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGTACTACTGGACTTGGATCCGCCAGACCCAGGGAAG 135

QY 124 GGCCTGAGTGGATGGGTACATCTATCAGTGGGAAACACCTACAAACCCGTCCTC 183
Db 136 GGCCTGAGTGGATGGGTTCATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 195

QY 184 AAGAGTCGAATGGCCATGTCCGTAGACACGCTCTGAGAACAGTTCTCCCTGAGGCTGAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACACGAGTTCTCCCTGAGGCTGAGC 255
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QY 244 TCTGTGACTGCGCGGACACGGCCGCTGTTACTGTTGGAGTTAGATGGCTACACTTTG 303
 Db 256 TCTGTGACTGCGCGGACACGGCCGCTGTTACTGTTGGAGTTAGATGGCTTTT 312
 QY 304 GACATCTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 342
 Db 313 GACTACTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 351
 RESULT 6
 ID ADD05390
 ADD05390 standard; DNA; 352 BP.
 XX
 AC ADD05390;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID NO 15.
 XX
 KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
 KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX W02003057006-A2.
 XX
 PD 17-JUL-2003.
 XX
 XX 26-DEC-2002; 2002WO-US041582.
 XX
 PR 28-DEC-2001; 2001US-0346460P.
 XX
 XX (ABGE-) ABGENIX INC.
 XX
 XX Gudas J, Bar-Eli M;
 PI
 PI WPI; 2003-577496/54.
 DR
 DR P-PSDB; ADD05388.
 XX
 XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
 PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
 PT associated with melanoma, or increasing survival of an animal having a
 PT metastatic tumor.
 XX
 XX Disclosure; SEQ ID NO 15; 87pp; English.
 PS
 XX The invention relates to a novel monoclonal antibody used for inhibiting
 CC tumour growth in an animal. The tumour inhibition process comprises
 CC selecting an animal in need of treatment for a tumour, providing a
 CC monoclonal antibody comprising a heavy chain amino acid, where the
 CC antibody consists of any one of 10 fully defined sequences of 117-123
 CC amino acids given in the specification, and where the monoclonal antibody
 CC binds MUC18, and contacting the tumour with the antibody resulting in
 CC inhibited proliferation of the cells. The monoclonal antibody has
 CC cytostatic and can be used in the production of a vaccine. The monoclonal
 CC antibodies against the MUC18 antigen are useful for diagnosing and
 CC treating tumors, inhibiting tumour growth (e.g. melanoma, lung tumour or
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
 CC increasing survival of an animal having a metastatic tumour. This
 CC polynucleotide sequence represents the DNA encoding an anti-MUC18
 CC antibody heavy chain, variable region, protein of the invention.
 XX
 SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;
 Query Match 80.4%; Score 275; DB 9; Length 352;
 Best Local Similarity 90.3%; Pred. No. 5e-69; Mismatches 3; Gaps 1;
 Matches 306; Conservative 0; Indels 30; Indels 3; Gaps 1;
 QY 4 GAGTGTGCGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
 Db 16 GAGTGTGCGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 75

QY 64 GCGGGCTCCATCCGACAGTGGTGGTACTACTGAGTTGGATCCGCCAACACCCAGGGAAG 123
 Db 76 GGTGGCTCCATCCGACAGTGGTGGTACTACTGAGTTGGATCCGCCAACACCCAGGGAAG 135
 QY 124 GGCTGGAGTGGATTGGGTACATCTATCAGTGGGAACACCTACAAACCCCTCCCTC 183
 Db 136 GGCTGGAGTGGATTGGGTTCATCTATTACGTGGGAGACCTACTACTACACCCCTCCCTC 195
 QY 184 AAGAGTCGAATTGCCATGTCCGTAGACACCTCTAGAACAAAGTTCTCCCTGAGGCTGAAC 243
 Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACAGATTCTCCCTGAAGCTGAGC 255
 QY 244 TCTGTGACTGCGCGGACACGGCCGCTGTTACTGTTGGAGTTAGATGGCTACACTTTG 303
 Db 256 TCTGTGACTGCGCGGACACGGCCGCTGTTACTGTTGGAGTTAGATGGCTTTT 312
 QY 304 GACATCTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 342
 Db 313 GACTACTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 351
 RESULT 7
 ID AAF29046
 AAF29046 standard; DNA; 369 BP.
 XX
 AC AAF29046;
 XX
 DT 03-APR-2001 (first entry)
 XX
 DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 2.
 XX
 KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
 KW envelope glycoprotein; gp120; diagnosis; ds.
 XX
 OS Homo sapiens.
 XX
 XX W0200100678-A1.
 XX
 PD 04-JAN-2001.
 XX
 XX 23-JUN-2000; 2000WO-US017327.
 PF
 PF 30-JUN-1999; 99US-0141701P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Watkins BA, Reitz MS;
 PI
 PI WPI; 2001-112438/12.
 DR
 DR P-PSDB; AAB62745.
 XX
 PT Novel human monoclonal antibody immunoreactive with human
 PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
 PT in biological sample and providing passive immunotherapy to HIV-1
 PT infected mammal.
 XX
 XX Claim 4; Page 34-35; 81pp; English.
 PS
 XX The present invention provides the protein and coding sequences for the
 CC variable regions of human monoclonal antibodies which are immunoreactive
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
 CC These can be used in diagnosis and therapy of HIV-1 infection
 XX
 SQ Sequence 369 BP; 75 A; 104 C; 107 G; 83 T; 0 U; 0 Other;
 Query Match 77.7%; Score 265.8; DB 4; Length 369;
 Best Local Similarity 87.5%; Pred. No. 2.2e-66; Mismatches 32; Indels 12; Gaps 1;
 Matches 307; Conservative 0; Indels 32; Indels 12; Gaps 1;
 QY 4 GAGTGTGCGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 63
 Db 19 GAGTGTGCGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGGCTGTCTCT 78

QY 64 GCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTTGGATCCGCAACACCCAGGGAAG 123
|||
Db 79 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTTGGATCCGCAACCCAGGGAAG 138
|||
QY 124 GGCCTGGAGTGGATGGGTACATCTATCATCAGTGGGAACACCTACAAACCCGTCCTTC 183
|||
Db 139 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACAAACCCGTCCTTC 198
|||
QY 184 AAGAGTCGAAATGGCCATGTCGGGTAGACACGCTCTGAGAACAAAGTTCTCCCTAGGCTGAAC 243
|||
Db 199 AAGAGTCGAGTTTACCATATCAATAGACACGCTCTAAGAACAAAGTTCTCCCTAGGCTGAGC 258
|||
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGG-----TTAGAT 291
|||
Db 259 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGGCGCGGTATTGTGGTGGT 318
|||
QY 292 GGTACACATTTGGACATCTGGGGCCAGGGAACCCCTGGTACCGTCTCTCTCA 342
|||
Db 319 GATTGCTCTTTGACTACTGGGGCCAGGGAACCCCTGGTACCGTCTCTCTCA 369
|||

RESULT 8

ID ADC99778 standard; DNA; 352 BP.

AC ADC99778;

DT 01-JAN-2004 (first entry)

DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 7.

XX Anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human; ds; gene.

OS Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041581.

PR 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

PI Gudas J;

XX WPI; 2003-587113/55.

DR P-PSDB; ADC99776.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.

PS Claim 8; SEQ ID NO 7; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumors, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 77.6%; Score 265.4; DB 9; Length 352;
Best Local Similarity 88.5%; Pred No. 2.9e-66;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCTGCGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCCTGTCTCT 63
|||
Db 16 GAGTCTGCGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCCTGTCTCT 75
|||
QY 64 GCGGCTCCATCCGCGAGTGGTGGTTACTACTGGAGTTGGATCCGCAACCCAGGGAAG 123
|||
Db 79 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTTGGATCCGCAACCCAGGGAAG 138
|||
QY 124 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACAAACCCGTCCTTC 183
|||
Db 139 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACAAACCCGTCCTTC 195
|||
QY 184 AAGAGTCGAAATGGCCATGTCGGGTAGACACGCTCTGAGAACAAAGTTCTCCCTAGGCTGAAC 243
|||
Db 199 AAGAGTCGAGTTTACCATATCAATAGACACGCTCTAAGAACAAAGTTCTCCCTAGGCTGAGC 255
|||
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGTGGATCCGCAACCCAGGGAAG 303
|||
Db 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGTGGATCCGCAACCCAGGGAAG 312
|||
QY 304 GACATCTGGGCGCCAGGGAACCCCTGGTACCGCTCTCTCTCA 342
|||
Db 313 AAGTACTGGGCGCCAGGGAACCCCTGGTACCGCTCTCTCTCA 351
|||

RESULT 9

ADD05382
ID ADD05382 standard; DNA; 352 BP.

AC ADD05382;

DT 01-JAN-2004 (first entry)

DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 7.

XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.

OS Homo sapiens.

XX WO2003057006-A2.

PN 17-JUL-2003.

PF 26-DEC-2002; 2002WO-US041582.

PR 28-DEC-2001; 2001US-0346460P.

XX (ABGE-) ABGENIX INC.

PI Gudas J, Bar-Eli M;

XX WPI; 2003-577496/54.

DR P-PSDB; ADD05380.

XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.

PS Disclosure; SEQ ID NO 7; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123

XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Bar-Eli M;
XX XX
DR WPI; 2003-577496/54.
DR P-PSDB; Add05400.
XX XX
PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX XX

PS Disclosure: SEQ ID NO 27; 87pp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting
XX tumour growth in an animal. The tumour inhibition process comprises
XX selecting an animal in need of treatment for a tumour, providing a
XX monoclonal antibody comprising a heavy chain amino acid, where the
XX antibody consists of any one of 10 fully defined sequences of 117-123
XX amino acids given in the specification, and where the monoclonal antibody
XX binds MUC18, and contacting the tumour with the antibody resulting in
XX inhibited proliferation of the cells. The monoclonal antibody has
XX cytostatic and can be used in the production of a vaccine. The monoclonal
XX antibodies against the MUC18 antigen are useful for diagnosing and
XX treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
XX tumour metastasis), inhibiting cell invasion associated with melanoma, or
XX increasing survival of an animal having a metastatic tumour. This
XX polynucleotide sequence represents the DNA encoding an anti-MUC18
XX antibody heavy chain, variable region, protein of the invention.

XX Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;

Query Match 77.5%; Score 265.2; DB 9; Length 358;
Best Local Similarity 88.0%; Pred. No. 3.3e-66;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGGGCTCTCT 63
Db 16 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGGGCTCTCT 75

QY 54 GCGGCTCCATCCGAGTGGTGGTTACTACTGGAGTGGATCCGCCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 135
QY 124 GGCCTGGAGTGGATGGGTACATCTATCACAGTGGGAAACACTCAACAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGGGTACATCTATTCAGTGGGAGCCTACTACAACCCGTCCTC 195
QY 184 AAGAGTCGAATTGCGAATGCGGTAGACACGCTGTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAATTACCTTATCAGTAGACACGCTTAAGAACCCAGTTCTCCCTGAGGCTGAAC 255
QY 244 TCTGTAGTCCGCGGACACGCGGTGTATTACTGTGGAG---GTTAGATGGGTACTACT 300
Db 256 TCTATGACTGCGCGGACACGCGGTGTATTACTGTGGAGAGATCGGGAAACAGCTGGT 315
QY 301 TTGACATCTCGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 316 TTGACTACTGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 357

RESULT 12
ID AAA46876
AC AAA46876 standard; DNA; 516 BP.

XX AAA46876;
XX AC
XX AC
XX 03-OCT-2000 (first entry)
XX DNA encoding the heavy chain of immunoglobulin clone 2.1.3.
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.

XX Homo sapiens.

XX WO200037504-A2.

XX 29-JUN-2000.

XX 23-DEC-1999; 99WO-US030895.

XX 23-DEC-1998; 98US-0113647P.

XX (PFIZ) PFIZER INC.

XX (ABGE-) ABGENIX INC.

XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;

XX Corvalan JR;

XX WPI; 2000-442647/38.

XX P-PSDB; AAY93713.

XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
XX -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.

XX Example 2; Fig 1G; 157pp; English.

XX The present sequence encodes a heavy chain of an antibody of the
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
XX -4. Antibodies of the invention are composed of a heavy chain variable
XX region, comprising a modified contiguous sequence from a FRI-FR3 sequence
XX encoded by a human VH3-33 family gene. The modifications are contained in
XX CDR1, CDR2 and/or framework regions. The antibodies may be used to
XX inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
XX disorders (e.g. autoimmune disease, diabetes and graft rejection) and
XX proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
XX used to up-regulate immune system to up-regulate immunodeficient
XX disorders

XX Sequence 516 BP; 103 A; 167 C; 142 G; 104 T; 0 U; 0 Other;

Query Match 76.3%; Score 260.8; DB 3; Length 516;
Best Local Similarity 87.4%; Pred. No. 6.7e-65;
Matches 299; Conservative 0; Mismatches 37; Indels 6; Gaps 1;

QY 7 TCTGGCCCGAGACTGGTGAAGCCTGCACAGACCTCTCCCTCAGCTGGCTGTCTCTGC 66
Db 1 TCGGGCCCGAGACTGGTGAAGCCTTCACAGATCCTGTCTCCCTCAGCTGTCTCTGT 60
QY 67 GGCCTCCATCCGACGTGGTGGTTACTACTGGAGTGGATCCGCCAACACCCAGGGAAGGC 126
Db 61 GGCCTCCATCAGCAGTGGTGGTCACTACTGGAGCTGGATCCGCCAGACCCAGGGAAGGC 120
QY 127 CTGAGTGGATGGGTACATCTATCAGTGGGGAACCTTACAACCCCTCCCTCAAG 186
Db 121 CTGAGTGGATGGGTACATCTATTAATTTGGGAACCTTACTACAACCCCTCCCTCAAG 180
QY 187 AGTCGAATGGCATGTCCGTAGACACGCTCTGAGAACAGTTCTCCCTGAGGCTGACTCT 246
Db 181 AGTCGAGTACCATATCAGTAGACACGCTCTAAGAACCCAGTTCTCCCTGAGGCTGACTCT 240
QY 247 GTGACTGCCGGGACACGGCCGTGTATTACTGTGGAGGTTAGATGG-----CTACACT 300
Db 241 GTGACTGCCGGGACACGGCCGTGTATTATTGTGGAGAGATAGTGGGACTACTACCGT 300
QY 301 TTGAGCATCTGGGGCCGAGGGAACCCCTGGTCAACCTGTCTCTCTCA 342
Db 301 ATAGACGTCTGGGGCCGAGGGAACCCAGGTCACCGTCTCTCTCTCA 342

RESULT 13
ADC99806

```

ID AC ADC99806 standard; DNA; 352 BP.
XX AC ADC99806;
XX DT 01-JAN-2004 (first entry)
XX DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 35.
XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX KW cytotatic; melanoma; oesophageal; pancreatic; colorectal tumour;
XX KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX KW lung cancer; human; ds; gene.
XX OS Homo sapiens.
XX PN WO2003057838-A2.
XX PD 17-JUL-2003.
XX XX 26-DEC-2002; 2002WO-US041581.
XX PF P-PSDB; ADC99804.
XX PR (ABGE-) ABGENIX INC.
XX PA Gudas J;
XX PI Claim 8; SEQ ID NO 35; 78pp; English.
XX CC The invention relates to a novel isolated monoclonal antibody comprising
XX CC a heavy or light chain amino acid or a heavy or light chain variable
XX CC domain where the antibody binds to MUC18. The monoclonal antibody of the
XX CC invention demonstrates cytostatic activity and may be useful for treating
XX CC a disease or condition associated with the expression of MUC18 on the
XX CC cell surface such as tumours, specifically melanoma, oesophageal,
XX CC pancreatic or colorectal tumours, carcinomas, particularly cervical
XX CC carcinomas and cervical intraepithelial neoplasia and cancers including
XX CC colorectal, breast or lung cancer, as well as other malignancies. The
XX CC current sequence is that of the anti-human MUC18 monoclonal antibody
XX CC heavy chain variable domain DNA of the invention.
XX SQ Sequence 352 BP; 77 A; 101 C; 105 G; 69 T; 0 U; 0 Other;

Query Match 75.0%; Score 256.4; DB 9; Length 352;
Best Local Similarity 87.0%; Pred. No. 1.1e-63;
Matches 294; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 5 AGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGCCTGCTCTCTG 64
DB 17 AGTGGGGGCCAGGACTGGTGAAGCCTTCAGAGACCCCTGTCCTCAGTGCCTGCTCTG 76
QY 65 GCGGCTCCATCCGACGAGTGGTGGTACTACTGGAGTTGGATCCGCAACACCCAGGAGG 124
DB 77 GTGGCTCCATCAGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 136
QY 125 GCCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 184
DB 137 GCCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 196
QY 185 AGATCGAATTCATGTCGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGTGACT 244
DB 197 AGATCGAATTCATGTCGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGTGACT 256
QY 245 CTGTGACTGCGCGACACGCGCGTGTATTACTGTGCGAGTTAGTGGCTPACACTTGG 304
DB 257 CTGTGACGCGCGCGACACGCGCGTGTATTACTGTGCGAGTTAGTGGCTPACACTTGG 313

QY 305 ACATCTGGGGCCAGGGAACCCCTGTCACCGTCTCCTCA 342
XX ACATCTGGGGCCAGGGAACCCCTGTCACCGTCTCCTCA 342
DB 314 GATACTGGGGCCAGGGAACCCCTGTCACCGTCTCCTCA 351
XX GATACTGGGGCCAGGGAACCCCTGTCACCGTCTCCTCA 351

RESULT 14
ADD05410
ID ADD05410 standard; DNA; 352 BP.
XX AC ADD05410;
XX DT 01-JAN-2004 (first entry)
XX DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 35.
XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO2003057006-A2.
XX PD 17-JUL-2003.
XX XX 26-DEC-2002; 2002WO-US041582.
XX PF P-PSDB; ADD05408.
XX PR 28-DEC-2001; 2001US-0346460P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Bar-Eli M;
XX PI Claim 8; SEQ ID NO 35; 87pp; English.
XX CC The invention relates to a novel monoclonal antibody used for inhibiting
XX CC tumour growth in an animal. The tumour inhibition process comprises
XX CC selecting an animal in need of treatment for a tumour, providing a
XX CC monoclonal antibody comprising a heavy chain amino acid, where the
XX CC antibody consists of any one of 10 fully defined sequences of 117-123
XX CC amino acids given in the specification, and where the monoclonal antibody
XX CC binds MUC18, and contacting the tumour with the antibody resulting in
XX CC inhibited proliferation of the cells. The monoclonal antibody has
XX CC cytostatic and can be used in the production of a vaccine. The monoclonal
XX CC antibodies against the MUC18 antigen are useful for diagnosing and
XX CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
XX CC increasing survival of an animal having a metastatic tumour. This
XX CC polynucleotide sequence represents the DNA encoding an anti-MUC18
XX CC antibody heavy chain, variable region, protein of the invention.
XX SQ Sequence 352 BP; 77 A; 101 C; 105 G; 69 T; 0 U; 0 Other;

Query Match 75.0%; Score 256.4; DB 9; Length 352;
Best Local Similarity 87.0%; Pred. No. 1.1e-63;
Matches 294; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 5 AGTCTGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGTGCCTGCTCTCTG 64
DB 17 AGTGGGGGCCAGGACTGGTGAAGCCTTCAGAGACCCCTGTCCTCAGTGCCTGCTCTG 76
QY 65 GCGGCTCCATCCGACGAGTGGTGGTACTACTGGAGTTGGATCCGCAACACCCAGGAGG 124
DB 77 GTGGCTCCATCAGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 136
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QY 125 GCCTGGAGTGGATTGGGTACATCTATCACAGTGGGAACACCTACAAACACCGTCCCTCA 184
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QY 185 AGAGTCGAATTCGCCATGTCGGTAGACAGCTGTGAGAACAAAGTTCTCCCTGAGGCTGAAC 244
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Db 197 AGAGTCGAATTCACCATATCAGTAGACACGCTCTAAGAACCCAGTTCTCCCTGAAGCTGAGCT 256
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QY 245 CTGTGACTGCCGCGACACGCGCGGTGTTACTGTGCGAGGTAGATGGCTACACTTTGG 304
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Db 257 CTGTGACTGCCGCGACACGCGCGGTGTTACTGTGCGAG--AGGGGAGATGGCTACA 313
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QY 305 ACATCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
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Db 314 GATACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 351
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RESULT 15

AAQ38670
ID AAQ38670 standard; cDNA; 357 BP.

XX AAQ38670;

XX 25-MAR-2003 (revised)

DT 06-MAY-1993 (first entry)

XX MAB GAH variable region of heavy chain.

XX Monoclonal antibody; hybridoma; PCR; variable region; constant region;
KW heavy chain; light chain; ss.

XX Synthetic.

XX EP520499-A1.

XX 30-DEC-1992.

XX 26-JUN-1992; 92EP-00110841.

XX 28-JUN-1991; 91JP-00158859.

PR 28-JUN-1991; 91JP-00158860.

PR 28-JUN-1991; 91JP-00158861.

XX (MITU) MITSUBISHI KASEI CORP.

XX Hosokawa S, Tagawa T, Hirakawa Y, Ito N, Nagaike K;

XX WPI; 1993-001328/01.

DR P-PSDB; AAR30143.

XX Human monoclonal antibody specific for a cancer cell membrane surface
PT antigen - prepnd. from a hybridoma obtd. by cell fusion between human
PT lymphocytes derived from cancer patients and mouse myeloma cells.

XX Claim 13; Page 31 + 14-15; 37pp; English.

XX A human MAb specifically binding to a surface antigen of cancer cell
CC membrane comprises variable regions of the heavy and light chains having
CC the amino acid sequences of AAR30143-44 respectively, encoded by DNA
CC sequences AAQ38670 and AAQ33032 respectively. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX Sequence 357 BP; 73 A; 105 C; 102 G; 77 T; 0 U; 0 Other;

Query Match 74.7%; Score 255.6; DB 2; Length 357;

Best Local Similarity 86.3%; Pred. NO. 1.9e-63;

Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 4 GAGTCTGCCGCCAGGACTGGTGAAGCTGCAGACCCCTGTCTCCCTCAGCTGGCTGTCTCT 63

Db 16 GAGTCTGCCGCCAGGACTGGTGAAGCTTCACAGACCCCTGTCTCCCTCAGCTGTCTCT 75

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QY 64 GCGGGCTCCATCCGCACTGGTGGTTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
    |||||
Db 76 GGTGGCTCCATCAGCAGTTTGGTTTCTACTGGAACTGGATCCGCCAGCACCAGGGAAG 135
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QY 124 GGCCTGGAGTGGATTGGGTACATCTATCACAGTGGGAACACCTACAAACACCGTCCCTC 183
    |||||
Db 136 GGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAAACCGTCCCTC 195
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QY 184 AAGATCGAATTTGCCATGTCGGTAGACACAGTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
    |||||
Db 196 AAGATCGAATTTACCATATCGCTAGACACAGTCTAAGAGCCAGTTCTCCCTGAAGCTGAGC 255
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QY 244 TCTGTGACTGCCGCGGACACGCGCGGTGTTACTGTGCGAGTTAGATGGCTACACTTTG 303
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Db 256 TCTGTGACTGCCGCGGACACGCGCGGTGTTACTGTGCGAGTTAGATGGCTACACTTTG 315
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QY 304 ---GACATCTGGGGCCAGGGAACCCCTGTCTCCCTCCTCA 342
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Db 316 GCTGACTACTGGGGCCAGGGAACCAATGGTCAACCGTCTCTTCA 357
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Job time : 226.818 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 03:58:10 ; Search time 760.173 Seconds

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Title: US-10-027-725A-1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	310	90.6	342	15	Sequence 1, Appli
3	298.8	87.4	342	15	Sequence 3, Appli
4	275	80.4	352	15	Sequence 2, Appli
5	275	80.4	352	15	Sequence 15, Appl
6	275	80.4	352	17	Sequence 15, Appl
7	265.4	77.6	352	15	Sequence 15, Appl
8	265.4	77.6	352	15	Sequence 7, Appli
9	265.2	77.5	358	15	Sequence 7, Appli
10	265.2	77.5	358	15	Sequence 27, Appl
11	265.2	77.5	358	17	Sequence 27, Appl
12	265.2	77.4	663	10	Sequence 27, Appl
13	264.6	77.4	370	16	Sequence 79, Appl
14	264.4	77.3	370	16	Sequence 189, App

15	262.2	76.7	361	16	US-10-309-762-191	Sequence 191, App
16	261.4	76.4	429	16	US-10-309-762-110	Sequence 110, App
17	259.6	75.9	370	16	US-10-309-762-186	Sequence 186, App
18	259.4	75.8	367	16	US-10-309-762-195	Sequence 195, App
19	256.4	75.0	352	15	US-10-330-613-35	Sequence 35, Appl
20	256.4	75.0	352	15	US-10-330-530-35	Sequence 35, Appl
21	256.4	75.0	352	17	US-10-660-357-35	Sequence 35, Appl
22	256.4	75.0	370	16	US-10-309-762-200	Sequence 200, App
23	255.2	74.6	376	16	US-10-309-762-187	Sequence 187, App
24	254.8	74.5	370	16	US-10-309-762-201	Sequence 201, App
25	254.8	74.5	370	16	US-10-309-762-212	Sequence 212, App
26	253.8	74.2	370	16	US-10-309-762-185	Sequence 185, App
27	253.6	74.2	376	16	US-10-309-762-184	Sequence 184, App
28	253.6	74.2	376	16	US-10-309-762-197	Sequence 197, App
29	253.6	74.2	376	16	US-10-309-762-199	Sequence 199, App
30	250.6	73.3	382	16	US-10-309-762-194	Sequence 194, App
31	249.4	72.9	352	16	US-10-309-762-203	Sequence 203, App
32	249.4	72.8	324	9	US-09-864-761-31244	Sequence 31244, A
33	248.4	72.6	519	16	US-10-309-762-174	Sequence 174, App
34	247.8	72.5	450	15	US-10-390-986-13	Sequence 13, Appl
35	245.8	71.9	381	17	US-10-312-316-64	Sequence 64, Appl
36	245.8	71.9	384	17	US-10-312-316-68	Sequence 68, Appl
37	244.2	71.4	381	17	US-10-312-316-66	Sequence 66, Appl
38	243	71.1	361	16	US-10-309-762-193	Sequence 193, App
39	241	70.5	1543	9	US-09-800-729-74	Sequence 74, Appl
40	240.4	70.3	333	9	US-09-925-299-198	Sequence 198, App
41	240.4	70.3	333	10	US-09-925-299-198	Sequence 198, App
42	239.2	69.9	378	9	US-09-974-449-5	Sequence 5, Appli
43	233.6	68.3	462	17	US-10-693-629-47	Sequence 47, Appl
44	230.6	67.4	349	12	US-10-269-711-2	Sequence 2, Appli
45	229.8	67.2	356	17	US-10-388-214A-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1

US-10-027-725A-1
; Sequence 1, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-1

Query Match 100.0%; Score 342; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.6e-101;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTCGAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCTGTCCTCAGCTGGCTGTC	60
Db	1	CTCGAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCTGTCCTCAGCTGGCTGTC	60
QY	61	TTTGGGGGCTCCATCCGACAGTGGTGTGTACTACTGTGAGTTGGATCCGCCAACACCCAGGG	120
Db	61	TTTGGGGGCTCCATCCGACAGTGGTGTGTGTACTACTGTGAGTTGGATCCGCCAACACCCAGGG	120
QY	121	AAGGGCTGGAGTGGATTGGGTACATCTATCAAGTGGGAACACCTACAAACACCCGTCC	180
Db	121	AAGGGCTGGAGTGGATTGGGTACATCTATCAAGTGGGAACACCTACAAACACCCGTCC	180
QY	181	CTCAAGATCGAATGCCATGTCGGTAGACACGTCTGTAGAACAAAGTTCTCCCTGAGGCTG	240

Db 181 CTCAGAGTCGAATGGCATGTCGGTAGACACGCTGAGAACAGTTCTCCCTGAGGCTG 240
Qy 241 AACTCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTACT 300
Db 241 AACTCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTACT 300
Qy 301 TTGGACATCTGGGCGCAGGGAACCTGTGTACCGTCTCTCTCA 342
Db 301 TTGGACATCTGGGCGCAGGGAACCTGTGTACCGTCTCTCTCA 342

RESULT 2

US-10-027-725A-3
; Sequence 3, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-3

Query Match 90.6%; Score 310; DB 15; Length 342;
Best Local Similarity 94.2%; Pred. No. 1.7e-90;
Matches 322; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGTCCCTCAGCTGCGCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCCTCAGCTGTC 60
Qy 61 TCTGCGGCTCATCCGAGTGGTGTACTACTGAGTTGATCGGCAACACCCAGG 120
Db 61 TCTGCGGCTCATCCGAGTGGTGTATTACTGAGTTGATCGGCAACCCAGG 120
Qy 121 AAGGCGCTGGAGTGGTGTACATCTATCAGTGGGAACACCTACAAACCCGTC 180
Db 121 AAGGCGCTGGAGTGGTGTACATCTATCAGTGGGAACACCTACAAACCCGTC 180
Qy 181 CTCAGAGTCGAATGGCATGTCGGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCGAATGGCATGTCGGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGCTG 240
Qy 241 AACTCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTACT 300
Db 241 AACTCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTACT 300
Qy 301 TTGGACATCTGGGCGCAGGGAACCTGTGTACCGTCTCTCTCA 342
Db 301 TTGGACATCTGGGCGCAGGGAACCTGTGTACCGTCTCTCTCA 342

RESULT 3

US-10-027-725A-2
; Sequence 2, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-2

Query Match 87.4%; Score 298.8; DB 15; Length 342;
Best Local Similarity 92.1%; Pred. No. 7.2e-87;
Matches 315; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGTCCCTCAGCTGCGCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCCTCAGCTGTC 60
Qy 61 TCTGCGGCTCATCCGAGTGGTGTACTACTGAGTTGATCGGCAACACCCAGG 120
Db 61 TCTGCGGCTCATCCGAGTGGTGTATTATTGAGTTGGTCCGCGCAGCTCCAGG 120
Qy 121 AAGGCGCTGGAGTGGTGTACATCTATCAGTGGGAACACCTACAAACCCGTC 180
Db 121 AAGGCGCTGGAGTGGTGTACATCTATCAGTGGGAACACCTACAAACCCGTC 180
Qy 181 CTCAGAGTCGAATGGCATGTCGGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCGAATGGCATGTCGGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGCTG 240
Qy 241 AACTCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGTTAGATGGCTACT 300
Db 241 AACTCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGGTTAGATGGCTACT 300
Qy 301 TTGGACATCTGGGCGCAGGGAACCTGTGTACCGTCTCTCTCA 342
Db 301 TTGGACATCTGGGCGCAGGGAACCTGTGTACCGTCTCTCTCA 342

RESULT 4

US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match 80.4%; Score 275; DB 15; Length 352;
Best Local Similarity 90.3%; Pred. No. 3.9e-79;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGGTGAAGCTGCACAGACCCCTGTCCCTCAGCTGCGCTGTC 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCCTCAGCTGTC 75
Qy 64 GCGGCTCATCCGAGTGGTGTACTACTGAGTTGATCGGCAACACCCAGGAG 123
Db 76 GGTGCTCATCAGCAGTGGTGTACTACTGAGTTGATCGGCAACACCCAGGAG 135
Qy 124 GGCCTGGAGTGGTGTACATCTATCAGTGGGAACACCTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGTGTACATCTATCAGTGGGAACACCTACTACAAACCCGTCCTC 195


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Db 136 GGCCTGAGTGGATGGGTACATCTATTACAGTGGGACCTACTACAACCCGTCCTC 195
Qy 184 AAGAGTCGAATGCGATGCGGTAGACACGCTTGAGAAAGTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTACAGACGCTTAAGAACCAAGTCTCCCTGAAGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 312
Qy 304 GACATCTGGGCGCAGGGAACCTGCTACCGTCTCCTCA 342
Db 313 AAGTACTGGGCGCAGGGAACCTGCTACCGTCTCCTCA 351

RESULT 8
US-10-330-530-7
; Sequence 7, Application US/10330530
; Publication No. US200301525141
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-7

Query Match 77.6%; Score 265.4; DB 15; Length 352;
Best Local Similarity 88.5%; Pred. No. 5.2e-76;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGCGCTGTCTCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGCGCTGTCTCT 75
Qy 64 GCGGCTCCATCCGAGTGGTGGTACTACTGAGTGGATCCGCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTACTTACCACCTGGAGCTGGATCCGCAACACCCAGGGAAG 135
Qy 124 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACAACACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACAACACCCGTCCTC 195
Qy 184 AAGAGTCGAATGCGATGCGGTAGACACGCTTGAGAAAGTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTACAGACGCTTAAGAACCAAGTCTCCCTGAAGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 312
Qy 304 GACATCTGGGCGCAGGGAACCTGCTACCGTCTCCTCA 342
Db 313 AAGTACTGGGCGCAGGGAACCTGCTACCGTCTCCTCA 351
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```
RESULT 9
US-10-660-357-7
; Sequence 7, Application US/10660357
; Publication No. US200401152051
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
```

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; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-7

Query Match 77.6%; Score 265.4; DB 17; Length 352;
Best Local Similarity 88.5%; Pred. No. 5.2e-76;
Matches 300; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGCGCTGTCTCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGCGCTGTCTCT 75
Qy 64 GCGGCTCCATCCGAGTGGTGGTACTACTGAGTGGATCCGCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTACTTACCACCTGGAGCTGGATCCGCAACACCCAGGGAAG 135
Qy 124 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACAACACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGGGTACATCTATCAGTGGGAACACCTACAACACCCGTCCTC 195
Qy 184 AAGAGTCGAATGCGATGCGGTAGACACGCTTGAGAAAGTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCAGTACAGACGCTTAAGAACCAAGTCTCCCTGAAGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGAGTTAGATGGCTACACTTTG 312
Qy 304 GACATCTGGGCGCAGGGAACCTGCTACCGTCTCCTCA 342
Db 313 AAGTACTGGGCGCAGGGAACCTGCTACCGTCTCCTCA 351

RESULT 10
US-10-330-613-27
; Sequence 27, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-27

Query Match 77.5%; Score 265.2; DB 15; Length 358;
Best Local Similarity 88.0%; Pred. No. 6e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGCGCTGTCTCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGCGCTGTCTCT 75
Qy 64 GCGGCTCCATCCGAGTGGTGGTACTACTGAGTGGATCCGCAACACCCAGGGAAG 123
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Db 76 GGTGGCTCCATCAACAGTGGTGGTGTCTACTGGAGCTGGATCGGCCAGCACCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATTGGGTACTATCATCAGTGGGAACACTACAACACCCGTCCTC 183
Db 136 GGCTGGAGTGGATTGGGTACTATCTTCCAGTGGGAGCACTACTACAACCCGTCCTC 195
Qy 184 AAGAGTCGAATTGGCATTCGGGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAATTACCTTATCAGTAGACACGCTCTAGAACCAAGTTCTCCCTGAAGCTGAAC 255
Qy 244 TCTGTGACTCGCGGACACCGCGGTGATTACTGTGCGAG---GTTAGATGGCTACACT 300
Db 256 TCTATGACTCGCGGACACCGCGGTGATTACTGTGCGAGAGATCGGGAACAGCTGGT 315
Qy 301 TTGGACATCTGGGCGCCAGGGAACCTGGTCAACCTCTCTCA 342
Db 316 TTTGACTACTGGGCGCCAGGGAACCTGGTCAACCTCTCTCA 357

RESULT 11

US-10-530-530-27
; Sequence 27, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX 031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-530-530-27

Query Match 77.5%; Score 265.2; DB 15; Length 358;
Best Local Similarity 88.0%; Pred. No. 6e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCAGACACCTGTCCCTCAGCTGGGTGTCTCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCCTGCAGACACCTGTCCCTCAGCTGGGTGTCTCT 75
Qy 64 GGCGGCTCCATCCGACGTGGTGTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGGTGTCTACTGGAGCTGGATCCGCCAGCACCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATTGGGTACTATCATCAGTGGGAACACTACAACACCCGTCCTC 183
Db 136 GGCTGGAGTGGATTGGGTACTATCTTCCAGTGGGAGCACTACTACAACCCGTCCTC 195
Qy 184 AAGAGTCGAATTGGCATTCGGGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAATTACCTTATCAGTAGACACGCTCTAGAACCAAGTTCTCCCTGAAGCTGAAC 255
Qy 244 TCTGTGACTCGCGGACACCGCGGTGATTACTGTGCGAG---GTTAGATGGCTACACT 300
Db 256 TCTATGACTCGCGGACACCGCGGTGATTACTGTGCGAGAGATCGGGAACAGCTGGT 315
Qy 301 TTGGACATCTGGGCGCCAGGGAACCTGGTCAACCTCTCTCA 342
Db 316 TTTGACTACTGGGCGCCAGGGAACCTGGTCAACCTCTCTCA 357

RESULT 12

US-10-660-357-27
; Sequence 27, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-27

Query Match 77.5%; Score 265.2; DB 17; Length 358;
Best Local Similarity 88.0%; Pred. No. 6e-76;
Matches 301; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCAGACACCTGTCCCTCAGCTGGGTGTCTCT 63
Db 16 GAGTCTGGCCAGGACTGGTGAAGCCTGCAGACACCTGTCCCTCAGCTGGGTGTCTCT 75
Qy 64 GGCGGCTCCATCCGACGTGGTGTACTACTGGAGTTGGATCCGCCAACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGGTGTCTACTGGAGCTGGATCCGCCAGCACCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATTGGGTACTATCATCAGTGGGAACACTACAACACCCGTCCTC 183
Db 136 GGCTGGAGTGGATTGGGTACTATCTTCCAGTGGGAGCACTACTACAACCCGTCCTC 195
Qy 184 AAGAGTCGAATTGGCATTCGGGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAATTACCTTATCAGTAGACACGCTCTAGAACCAAGTTCTCCCTGAAGCTGAAC 255
Qy 244 TCTGTGACTCGCGGACACCGCGGTGATTACTGTGCGAG---GTTAGATGGCTACACT 300
Db 256 TCTATGACTCGCGGACACCGCGGTGATTACTGTGCGAGAGATCGGGAACAGCTGGT 315
Qy 301 TTGGACATCTGGGCGCCAGGGAACCTGGTCAACCTCTCTCA 342
Db 316 TTTGACTACTGGGCGCCAGGGAACCTGGTCAACCTCTCTCA 357

RESULT 13

US-09-972-656-79
; Sequence 79, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Teai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(663)
US-09-972-656-79

Query Match 77.4%; Score 264.6; DB 10; Length 663;
Best Local Similarity 86.9%; Pred. No. 1.1e-75;
Matches 291; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY	4	GAGTCTGGCCGAGGACTGGTGAAGCTGCGACAGACCCCTGTCCCTCAGCTGGCGTGTCTCT	63
Db	16	GAGTCTGGCGCCGAGGACTGGTGAAGCCCTTCGGAGACCCCTGTCCCTCAGCTGGCGTGTCTCT	75
QY	64	GGCGGCTCCATCCGACAGTGGTGGTTACTACTGGAGTTGGATTCGCGCAACACCCAGGGGAAG	123
Db	76	GGTGGCTCCATCAGCAGTGGTGGTTACTCTTGGAGCTGGATCCGCGACGCCACGAGGAAG	135
QY	124	GGCCTGGAGTGGATTGGGTGATCATCTATCCACAGTGGGAAACACTTACAAACAACCCGTCCCTC	183
Db	136	GGCCTGGAGTGGATTGGGTGATCATCTATCATATGTTGGGAGCAGCTACTACAACCCGTCCCTC	195
QY	184	AAGAGTTCGAAATGGCAATCTCGGTAGACACGCTCTGAGAAACAAGTTCTCCCTCAGGCTGAAC	243
Db	196	AAGASTCGAGTCACCAATATCAGTAGACAGGTCGAAGAACCAAGTTCTCCCTGAAGCTGAGC	255
QY	244	TCTGTGACTGCCGGGACACGGCCGTGTATTACTGTGCGAGGTTAGATGGCTACACTTTTG	303
Db	256	TCTGTGACCGCCGGGACACGGCCGTGTATTACTGTGCGAGGGGACTGGGGCTACTTTT	315
QY	304	GACATCTGGGGCCAGGGAACCTGGTCAACCGCTCTC	338
Db	316	GACTACTTGGGGCCAGGGAACCTTGTCAACCGCTCTC	350

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RESULT 14
US-10-309-762-189
; Sequence 189, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYC ANHYDRASE IX
; FILE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-189

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Query Match	77.3%	Score 264.4;	DB 16;	Length 370;
Best Local Similarity	87.0%;	Prod. No. 1.1e-75;		
Matches 308; Conservative	0;	Mismatches 31;	Indels 15;	Gaps 1;
QY	4	GAGTCTGCCCCAGACACTGGTGAAGCGCTGCACAGACCCCTGTCCCTCAGCTGCGCTGTCTCT	63	
DB	16	GAGTGGGCCACAGACTGGTGAAGCCTTCAAGACCCCTGTCCCTCACTGCACCTGTCTCT	75	
QY	64	GGCGGCTCCATCCGAGTGGTGGTTACTATGGAGTTGGATCCGGCAACACCCAGGGAAG	123	
DB	76	GGTGGCTCCATCAGCAGTGGTGGTTACTATGGAGCTGGATCCGCCACACCCAGGGAAG	135	
QY	124	GGCCTGGAGTGGATTGGGTATACCTATCACAGTGGGAACACTACAAACCCGCTCCCTC	183	
DB	136	GGCCTGGAGTGGATTGGGTATACCTATTCACAGTGGGACCACTACTACAAACCCGCTCCCTC	195	
QY	184	AAGAGTCGAATTGCCATCTCGGTAGACACAGCTCTGAGACAGTTCTCCCTCAGAGCTGAAC	243	
DB	196	AAGAGTCGAGTTACCATATCAGTAGACACAGCTTAAGAACCAGTTCTCCCTGAAGCTGAGC	255	
QY	244	TCTGTACTGCCCGGACACGGCCGTGTATTACTGTGCGAGTTA-----	288	
DB	256	TCTGTGATCGCCGCGGACACGGCCGTGTATTACTGTGCGAGATTACTATGGTTCCGG	315	

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QY      289 GATGGCTACACTTTGGACATCTGGGCGCACGGBRACCCTGGTCAACGGTCTCCTCA 342
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db      316 GAAGACTACGGTGTTGGACGTCTGGGGCCAAAGGGACCACGGTCAACGGTCTCCTCA 369

RESULT 15
US-10-309-762-191
; Sequence 191, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;   APPLICANT: Gudus, Jean
;   APPLICANT: Foltz, Ian
;   APPLICANT: Handa, Masahisa
;   APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ARGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-191

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Query Match	76.7%	Score 262.2	DB 16	Length 361
Best Local Similarity	87.2%	Pred. No. 5.7e-75		
Matches 301	Conservative 0	Mismatches 38	Indels 6	Gaps 1
QY	4	GAGTCTGGCCAGACACTGGTGAAGCCCTGCACAGACCCCTGTCCCTCAGCTGGCGTGTCTCT	63	
Db	16	GAGTGGGGCCGAGACTGGTGAAGCCTTCAAGACCCCTGTCCCTCACTGCACACTGTCTCT	75	
QY	64	GGCGGCTCCATCCGACAGTGGTGGTTTACTTACTGGAGTTGGATCCGCGCAACACCCAGGGGAAG	123	
Db	76	GGTGGCTCCATCAGCAGTGGTGGTTTACTTACTGGAGTGGATCCGCGCAGCACCCAGGGGAAG	135	
QY	124	GGCCTGAGTGGAATGGGTGATCATCTATCAGACTGGGAACACTACAAACCCGTCCTC	183	
Db	136	GGCCTGGAGTGGATTTGGGTGATCTATTACAGTGGGAGTACTACTACAACCCGTCCTC	195	
QY	184	AAGAGTCGAATTTGCCATGTGGTGTAGACACGCTCAGAAACAAGTTCTCCCTCAGGCTGAAC	243	
Db	196	AAGAGTCGAGTTTACCATATCAGTTAGACACGCTTAGAACACAGTTCTCCCTGAAGCTGAGC	255	
QY	244	TCTGTGACTGCGGGGACACGGCCGGTGTATTACTGTGCGA-----GGTTAGATGGCTAC	297	
Db	256	TCTGTGACTGCGGGGACACGGCCGGTGTATTACTGTGCGAGAGATGGCTACAATTACTTGG	315	
QY	298	ACTTTGGACATCTGGGGCCAGGGAACCCCTGGTCAACCTCTCTCTCA	342	
Db	316	TACTTCGATCTCTGGGCGGTGGGACCCCTGGTCACTGTCTCTCTCA	360	

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Job time : 761.173 secs

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:21:37 ; Search time 48.3636 Seconds
(without alignments)
3924.296 Million cell updates/sec

Title: US-10-027-725

Perfect score:

Sequence: 1 ctcgagtctggcccaggact.....ccctggtcaccgtctcctca 342

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Maximum DB seq length: 200000000
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*

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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6A_COMB.seq:
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4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
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3: /cgn2_6/ptodata/2/lna/PC1US COMB.see
6: /cgn2_6/ptodata/2/lna/bac'fil.es1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

CONFIDENTIAL

Result No.	Score	Query Match	Length	DB	ID	Description
1	260.8	76.3	516	4	US-09-472-087-33	Sequence 33, Appl
2	255.6	74.7	357	1	US-08-360-125-3	Sequence 3, Appl
3	255.6	74.7	357	2	US-08-450-578-3	Sequence 3, Appl
4	255.6	74.7	357	2	US-09-017-628-3	Sequence 3, Appl
5	255.6	74.7	357	2	US-09-014-880-3	Sequence 3, Appl
6	255.6	74.7	357	4	US-08-450-363-3	Sequence 3, Appl
7	249	72.8	631	3	US-08-545-809A-31	Sequence 17, Appl
8	248.6	72.7	1567	3	US-09-049-672A-17	Sequence 17, Appl
9	247.8	70.5	450	4	US-09-582-337-13	Sequence 13, Appl
10	241	70.5	1543	4	US-09-800-729-74	Sequence 74, Appl
11	237	69.3	366	1	US-08-360-125-9	Sequence 9, Appl
12	237	69.3	366	2	US-08-450-578-9	Sequence 9, Appl
13	237	69.3	366	2	US-09-017-628-9	Sequence 9, Appl
14	237	69.3	366	2	US-09-014-880-9	Sequence 9, Appl
15	237	69.3	366	4	US-08-450-363-9	Sequence 9, Appl
16	228.2	66.7	1212	3	US-08-545-809A-61	Sequence 61, Appl
17	225	65.8	800	3	US-08-545-809A-39	Sequence 39, Appl
18	219.2	64.1	288	3	US-08-851-362D-7	Sequence 7, Appl
19	218.4	63.9	403	3	US-09-042-353-357	Sequence 357, App
20	218.4	63.9	403	4	US-08-758-417A-205	Sequence 205, App
21	218.2	63.8	840	3	US-09-260-527-4	Sequence 4, Appl
22	217.8	63.7	291	3	US-08-851-362D-11	Sequence 11, Appl
23	215.6	63.0	750	4	US-10-039-785-62	Sequence 62, Appl
24	213	62.3	357	2	US-08-652-818A-20	Sequence 20, Appl
25	212	62.0	291	3	US-08-855-1362D-9	Sequence 9, Appl
26	211	61.7	800	3	US-08-545-809A-55	Sequence 55, Appl
27	209.6	61.3	294	3	US-08-851-362D-3	Sequence 3, Appl

Qy 301 TTGGACATCTGGGGCCAGGGAACCTGGTCAACCGTCTCTCTCA 342
Db 301 ATAGACGTCTGGGGCCAGGGAACCGTCAACCGTCTCTCTCA 342

RESULT 2
US-08-360-125-3
; Sequence 3, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAF
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:

CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-3
Query Match 74.7%; Score 255.6; DB 1; Length 357;
Best Local Similarity 86.3%; Pred. No. 2e-70; 44; Indels 3; Gaps 1;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;
QY 4 GAGTCTGGCCCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGGCTCTCT 63
Db 16 GAGTGGGGCCCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGGCTCTCT 75
QY 64 GCGGCTCATCCGCGAGTGGTGTACTATGAGATTGATCCGCGAACACCCAGGGAAG 123
Db 76 GGTGGCTCATCAGCAGTTGTGGTTTCTACTGGAATGGATCCGCGAGCAGCCAGGGAAG 135
QY 124 GCGCTGGAGTGGATTGGGTAGATCTATCAGCTGGGAGACACCTACAAACCCGTCCTC 183
Db 136 GCGCTGGAGTGGATTGGGTAGATCTATCAGCTGGGAGACACCTATACAGCCGTCCTC 195
QY 184 AAGAGTCGAATTGCCATGTCCGTAGACACGCTGTGAGAACAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCGCTAGACAGCTTAAGAGCCAGTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGAGACACGCGCGGTATTACTGTGGAGGTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGCGGAGACACGCGCGGTATTACTGTGGAGGTACTACCCGACTACGGGG 315
QY 304 ---GACATCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACATGGTCAACCGTCTCTCTCA 357

RESULT 3
US-08-450-578-3
; Sequence 3, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,578
 FILING DATE: May 25, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/360,125
 FILING DATE: December 20, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/905,534
 FILING DATE: June 29, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8850
 TELEFAX:
 TELEX:
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL:
 ANTI-SENSE:
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM:
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Hybridoma producing human
 CELL TYPE: antibody GAH
 CELL LINE:
 ORGANELLE:
 IMMEDIATE SOURCE:
 LIBRARY:
 CLONE:
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT:
 MAP POSITION:
 UNITS:
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-450-578-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;
 Best Local Similarity 86.3%; Pred. No. 2e-70;
 Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGGCGTGTCTCT 63
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 Db 16 GAGTCGGGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGGCGTGTCTCT 75
 |||||
 QY 64 GCGGCTCCATCCCGCAGTGGTGTACTACTGGAGTTGGATCCGCCACACCCAGGGAAG 123
 |||||
 Db 76 GGTGGCTCCATCAGCAGTGTGGTTTCTACTGGAACTGGATCCGCCACACCCAGGGAAG 135
 |||||
 QY 124 GGCCTGGAGTGGATTGGGTACATCTATCACAGTGGGAACACTACAAACCCGTCCTC 183
 |||||
 Db 136 GGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGACCACTACTACACCCGTCCTC 195
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 QY 184 AAGAGTCGAATTGCCATGTGCGGTAGACACAGTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
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 Db 196 AAGAGTCGAGTTACCATATCGCTAGACACGCTTAAGAGCCAGTTCTCCCTGAAGCTGAGC 255
 |||||
 QY 244 TCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGGAGTTAGATGGGTACACTTTG 303
 |||||
 Db 256 TCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGGAGTTTACCCGACTAGGGGG 315
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 QY 304 ---GACATCTGGGGCCAGGGAACCCCTGCTCACCCTCTCTCTCA 342
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 Db 316 GCTGACTACTGGGCGCCAGGGAACAATGGTCACCGTCTCTTCA 357
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RESULT 4

US-09-017-628-3
 ; Sequence 3, Application US/09017628
 ; Patent No. 5990287
 ; GENERAL INFORMATION:
 ; APPLICANT: HOSOKAWA, Saiko
 ; APPLICANT: TAGAWA, Toshiaki
 ; APPLICANT: HIRAKAWA, Yoko
 ; APPLICANT: ITO, No. 5990287ihiko
 ; APPLICANT: NAGAIKE, Kazuhiro
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
 ; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
 ; FILE REFERENCE: 177/527361KH
 ; CURRENT APPLICATION NUMBER: US/09/017,628
 ; CURRENT FILING DATE: 1998-02-02
 ; EARLIER APPLICATION NUMBER: 08/360,125
 ; EARLIER FILING DATE: 1994-12-20
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 357
 ; TYPE: DNA
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Hybridoma producing human antibody GAH
 US-09-017-628-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;
 Best Local Similarity 86.3%; Pred. No. 2e-70;
 Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGGCGTGTCTCT 63
 |||||
 Db 16 GAGTCGGGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGGCGTGTCTCT 75
 |||||
 QY 64 GCGGCTCCATCCCGCAGTGGTGTACTACTGGAGTTGGATCCGCCACACCCAGGGAAG 123
 |||||
 Db 76 GGTGGCTCCATCAGCAGTGTGGTTTCTACTGGAACTGGATCCGCCACACCCAGGGAAG 135
 |||||
 QY 124 GGCCTGGAGTGGATTGGGTACATCTATCACAGTGGGAACACCTACAAACCCGTCCTC 183
 |||||
 Db 136 GGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 195
 |||||
 QY 184 AAGAGTCGAATTGCCATGTGCGGTAGACACGCTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
 |||||
 Db 196 AAGAGTCGAGTTACCATATCGCTAGACACGCTTAAGAGCCAGTTCTCCCTGAGCTGAGC 255
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 QY 244 TCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGGAGGTTAGATGGGTACACTTTG 303
 |||||

Db 256 TCTCTGACTGCGGGACACGGCGGTGATTACTGTGGAGGTCTACCCGACTACGGGG 315
Qy 304 ---GACATCTGGGCGGAGGAAACCTGTGTACCGGTCTCTCA 342
Db 316 GCTGACTACTGGGCGGAGGAAACATGTGTACCGGTCTCTCA 357

RESULT 5
US-09-014-880-3
; Sequence 3, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
US-09-014-880-3

Query Match 74.7%; Score 255.6; DB 2; Length 357;
Best Local Similarity 86.3%; Pred. No. 2e-70;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;
Qy 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCGTGTCT 63
Db 16 GAGTCGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGCGTGTCT 75
Qy 64 GCGGCTCCATCCGCGAGTGGTGTACTACTGAGTGGATCGCCACACCCAGGGAAG 123
Db 76 GGTGGTCCATCAGCAGTGTGTGTTTCTACTGGAAGTGGATCGCCAGGAGG 135

Qy 124 GGCCTGAGTGGATTGGGTACATCTATCAGTGGGAACACTACAAACCCGTCCTC 183
Db 136 GGCCTGAGTGGATTGGGTACATCTATTACAGTGGGACCTACTACAACCCGTCCTC 195
Qy 184 AAGAGTCGAATTGCCATGTCCGTAGACACGTCTGAGAAACAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCGTCTAGACACAGTCTAAGAGCCAGTTCTCCCTGAAGCTGAGC 255
Qy 244 TCTGTGACTGCGGCGGACACGGCGGTGATTACTGTGGAGGTAGATGGCTACACTTTG 303
Db 256 TCTGTGACTGCGGCGGACACGGCGGTGATTACTGTGGAGGTCTACCCGACTACGGGG 315
Qy 304 ---GACATCTGGGCGGAGGAAACCTGTGTACCGGTCTCTCA 342
Db 316 GCTGACTACTGGGCGGAGGAAACATGTGTACCGGTCTCTCA 357

RESULT 6
US-08-450-363-3
; Sequence 3, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

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; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:

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US-08-450-363-3

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Query Match          74.7%; Score 255.6; DB 4; Length 357;
Best Local Similarity 86.3%; Pred. No. 2e-70;
Matches 295; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

Qy 4 GAGTCTGCCAGACTGGTGAAGCCCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 63
Db 16 GAGTCGGGCCAGGACTGGTGAAGCCCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 75
Qy 64 GGCGGCTCCATCCCGAGTGGTGTACTACTGGAGTTGGATCCGCCACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTTGGTGTCTACTTGGAACTGGATCCGCCAGCACCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATTGGGTATCATCTATCACAGTGGGAACACCTACAAACCCCTGCCCTC 183
Db 136 GGCTGGAGTGGATTGGGTATCATCTATCACAGTGGGAACACCTACAAACCCCTGCCCTC 195
Qy 184 AAGAGTCGAATTGCCATGTCCGTAGACACGCTCTGAGAACCAAGTTCTCCCTGAGGCTGAAC 243
Db 196 AAGAGTCGAGTTACCATATCGCTAGACACGCTCTAAGAGCCAGTTCTCCCTGAAGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACAGCGCGGTGTATCTACTGTGGAGTTAGATGGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACAGCGCGGTGTATCTACTGTGGAGTTAGATGGTACACTTTG 315
Qy 304 ---GACATCTGGGGCCAGGGAACCCCTGGTCAACCTGTCCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACCAATGGTACCGTCTCTTCA 357

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RESULT 7

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US-08-545-809A-31
; Sequence 31, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

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; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 631 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
; US-08-545-809A-31

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Query Match          72.8%; Score 249; DB 3; Length 631;
Best Local Similarity 92.9%; Pred. No. 3e-68;
Matches 261; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 4 GAGTCTGCCAGACTGGTGAAGCCCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 63
Db 305 GAGTCGGGCCAGGACTGGTGAAGCCCTGCACAGACCCCTGTCCTCAGCTGGCTGTCTCT 364
Qy 64 GGCGGCTCCATCCCGAGTGGTGTACTACTGGAGTTGGATCCGCCACACCCAGGGAAG 123
Db 365 GGTGGCTCCATCAGCAGTTGGTGTACTACTGGAGTGGATCCGCCAGCACCCAGGGAAG 424
Qy 124 GGCTGGAGTGGATTGGGTATCATCTATCACAGTGGGAACACCTACACACCCGTCCTC 183
Db 425 GGCTGGAGTGGATTGGGTATCATCTATCACAGTGGGAACACCTACTACTACACCCGTCCTC 484
Qy 184 AAGAGTCGAATTGCCATGTCCGTAGACACCTCTGAGAACCAAGTTCTCCCTGAGGCTGAAC 243
Db 485 AAGAGTCGAGTTACCATATCAGTAGACACCTCTAAGAACCAAGTTCTCCCTGAGGCTGAGC 544
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Db 545 TCTGTGACTGCGCGGACAGCGCGGTGTATCTACTGTGGAG 585

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RESULT 8

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US-09-049-672A-17
; Sequence 17, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti

```

APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANTUT01
CLONE: 1513264
US-09-049-672A-17

Query Match 72.7%; Score 248.6; DB 3; Length 1567;
Best Local Similarity 84.0%; Pred. No. 5.7e-68;
Matches 300; Conservative 0; Mismatches 39; Indels 18; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGCGCTGTCTCT 63
Db 150 GAGTGGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCTCAGCTGCGCTGTCTCT 209
QY 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTGGATCGGCAACACCCAGGGAAG 123
Db 210 GTTGGCTCCATCACTAGTGGTGTACTACTGGAGCTGGATCGGCAACCCAGGGAAG 269
QY 124 GGCCTGGAGTGGATTGGTACATCTATCAGTGGGAACACCTACACACCCGTCCTC 183
Db 270 GGCCTGGAGTGGATTGGTACATCTATCAGTGGGAACACCTACACCCGTCCTC 329
QY 184 AGAGTCGAATTGCCATGTCGGTACAGCTCTGAGAACAAAGTTCCTCCCTGAGGCTGAAC 243
Db 330 AGAGTCGAATTGCCATGTCGGTACAGCTCTGAGAACAAAGTTCCTCCCTGAGGCTGAGC 389
QY 244 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGGTAGATG----- 292
Db 390 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGAGATGAGTGTAAAGG 449
QY 293 -----GTACACTTTGGACACTGGGGCCAGGGAACCTGTGACCGTCTCCTCA 342
Db 450 GGGGGGAACCTACCGGTATGGACGCTGGGGCCAGGGAACCTGTGACCGTCTCCTCA 506

RESULT 9

US-09-582-337-13
; Sequence 13, Application US/09582337
; Patent No. 6362618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(450)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: V_region
; LOCATION: (59)..(353)
US-09-582-337-13

Query Match 72.5%; Score 247.8; DB 4; Length 450;
Best Local Similarity 85.7%; Pred. No. 6.1e-68;
Matches 306; Conservative 0; Mismatches 32; Indels 19; Gaps 2;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCTCAGCTGCGCTGTCTCT 63
Db 74 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGT-CCTCACCTGCACTGTCTCT 132
QY 64 GCGGCTCCATCCGAGTGGTGTACTACTGGAGTTGGATCGGCAACACCCAGGGAAG 123
Db 133 GGTGGCTCCATCAGCAGTGGTGTACTACTGGAGCTGGATCGGCAACCCAGGGAAG 192
QY 124 GGCCTGGAGTGGATTGGGTACATCTATCAGTGGGAACACCTACAAACCCGTCCTC 183
Db 193 GGCCTGGAGTGGATTGGGTACATCTATCAGTGGGAACACCTACTACAAACCCGTCCTC 252
QY 184 AGAGTCGAATTGCCATGTCGGTACAGCTCTGAGAACAAAGTTCCTCCCTGAGGCTGAAC 243
Db 253 AAGAGTCGAATTGCCATGTCGGTACAGCTCTGAGAACAAAGTTCCTCCCTGAGGCTGAGC 312
QY 244 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGGT----- 286
Db 313 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGGTATTACTATGATAGTGT 372
QY 287 -TAGATGGCTACACTTTGGACATCTGGGCGCCAGGGAACCCCTGTGACCGTCTCCTCA 342
Db 373 GGTATTACGACTACTTTGACTACTGGGCGCCAGGGAACCCCTGTGACCGTCTCCTCA 429

RESULT 10

US-09-800-729-74
; Sequence 74, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044PI
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22


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; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-800-729-74

Query Match      70.5%; Score 241; DB 4; Length 1543;
Best Local Similarity 82.2%; Pred. No. 1.3e-65;
Matches 277; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCCTGCAGACCCCTGTCCCTCAGCTCGGTGTCTCT 63
Db 90 GAGTCGGGCCAGGACTGGTGAAGCCCTTCAGAGACCCCTGTCCCTCAGCTCGGTGTCTCT 149
QY 64 GCGGGCTCCATCCGAGTGGTGTACTACTGAGTGGATCGGCACACACCCAGGGAAG 123
Db 150 GGTGGCTCCATCAGCAGTGGTGTACTACTGAGTGGATCGGCACACCCAGGGAAG 209
QY 124 GCGCTGAGTGGATTTGGTTACATCTATCACAGTGGGAAACACCTACAAACCCGTCCTC 183
Db 210 GGCCTGAGTGGATTTGGTTACATCTTTACAAATGGGTCACTACTACATCGTCCCTC 269
QY 184 AAGAGTCGAATTCGATGTCGGTAGACACCTCTGAGAACAAAGTTCCTCGAGGCTGAAC 243
Db 270 AAGAGTCGAGTTACCATATCTGTAGACACGCTCTCAGAACCAAGTTCCTCGAGGCTGAGC 329
QY 244 TCTGTGACTCCCGGACACGCGGTGTATCTACTGTCGAGTGTAGATGGCTACACTTTG 303
Db 330 TCTGTGACTCCCGGACACGCGGTGTATCTACTGTCGAAAGATCATCGAGCGACAGA 389
QY 304 GACATCTGGGCCAGGAAACCCCTGGTCACCGCTCTCCT 340
Db 390 GACGGGTACCAGTGGGAATACCGAGGCTTTGACTACT 426

RESULT 11
US-08-360-125-9
; Sequence 9, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
```

```
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody 1-3-1
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-360-125-9

Query Match      69.3%; Score 237; DB 1; Length 366;
Best Local Similarity 82.3%; Pred. No. 1.3e-64;
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCCTGCAGACCCCTGTCCCTCAGCTCGGTGTCTCT 63
Db 16 GAGTCGGGCCAGGACTGGTGAAGCCCTTCGAGACCCCTGTCCCTCAGCTCGGTGTCTCT 75
QY 64 GCGGGCTCCATCCGAGTGGTGTACTACTGAGTGGATCGGCACACACCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGTAGTTACTACTGCGGTGGATCGGCACACCCAGGGAAG 135
QY 124 GCGCTGAGTGGATTTGGTTACATCTATCACAGTGGGAAACACCTACAAACCCGTCCTC 183
Db 136 GCGCTGAGTGGATTTGGGTAGTATCTATTATAGTGGGAGCACCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTTGCCATGTCCGTAGACACCTCTGAGAACCAAGTTCCTCGAGGCTGAAC 243
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EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 366
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-9

Query Match 69.3%; Score 237; DB 2; Length 366;
Best Local Similarity 82.3%; Pred. No. 1.3e-64;
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAGTCTGCGCCAGGACTGGTGAAGCCTGCACAGACCCCTGCTCCCTCAGCTGGCTGTCTCT 63
DB 16 GAGTCTGCGCCAGGACTGGTGAAGCCTGCAGAGACCCCTGCTCCCTCAGCTGTCTCT 75

QY 64 GCGGCTCCATCCCGAGTGGTGTACTTACTGAGTGGATCCGCGCAACCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTAGTGTACTTACTGAGTGGATCCGCGCAACCCAGGGAAG 135

QY 124 GCGCTGGAGTGGATTGGTGTACTTATCAGAGTGGGACACCTACCAACCCCTCCCTC 183
DB 136 GGGCTGGAGTGGATTGGGAGTATCTATTATAGTGGGACCTACTACTCAACCCCTCCCTC 195

QY 184 AAGAGTCCGATTCGCTGCTAGACACGCTGTGAGAACCAAGTTCCTCCCTGAGGCTGAAC 243
DB 196 AAGAGTCCGATTCACCATATCCGTTAGACACGCTCCAGAACCAAGTTCCTCCCTGAGGCTGAGC 255

QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGA-----GGTTAGAT 291
DB 256 TCTGTGACCGCGCAGACACGCGTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC 315

QY 292 GGCTACACTTTGGACATCTGGGGCAGGGAACCCCTGTCACCGTCTCTCA 342
DB 316 TACTACGGTATGGAGCTGTGGGGCCNAGGACACCGGTACCGGTCTCTCA 366

RESULT 14
US-09-014-880-9
Sequence 9, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-9

Query Match 69.3%; Score 237; DB 2; Length 366;
Best Local Similarity 82.3%; Pred. No. 1.3e-64;
Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAGTCTGCGCCAGGACTGGTGAAGCCTGCACAGACCCCTGCTCCCTCAGCTGGCTGTCTCT 63
DB 16 GAGTCTGCGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGCTCCCTCAGCTGTCTCT 75

QY 64 GCGGCTCCATCCCGAGTGGTGTACTTACTGAGTGGATCCGCGCAACCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTAGTGTACTTACTGAGTGGATCCGCGCAACCCAGGGAAG 135

QY 124 GCGCTGGAGTGGATTGGTGTACTTATCAGAGTGGGACACCTACCAACCCCTCCCTC 183
DB 136 GGGCTGGAGTGGATTGGGAGTATCTATTATAGTGGGACCTACTACTCAACCCCTCCCTC 195

QY 184 AAGAGTCCGATTCGCTGCTAGACACGCTGTGAGAACCAAGTTCCTCCCTGAGGCTGAAC 243
DB 196 AAGAGTCCGATTCACCATATCCGTTAGACACGCTCCAGAACCAAGTTCCTCCCTGAGGCTGAGC 255

QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGA-----GGTTAGAT 291
DB 256 TCTGTGACCGCGCAGACACGCGTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC 315

QY 292 GGCTACACTTTGGACATCTGGGGCAGGGAACCCCTGTCACCGTCTCTCA 342
DB 316 TACTACGGTATGGAGCTGTGGGGCCNAGGACACCGGTACCGGTCTCTCA 366

RESULT 15
US-08-450-363-9
Sequence 9, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434/hiho ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:
MAP POSITION:

FEATURE:

NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-363-9

Query Match 69.3%; Score 237; DB 4; Length 366;

Best Local Similarity 82.3%; Pred. No. 1.3e-64;

Matches 289; Conservative 0; Mismatches 50; Indels 12; Gaps 1;

QY 4 GAGTCGGCCAGGACTGGTGAAGCCTGCACAGACCCCTGTCCCTCAGCTGGCTGTCTCT 63

DB 16 GAGTCGGCCAGGACTGGTGAAGCCTGCAGACCCCTGTCCCTCAGCTGTCTCT 75

QY 64 GGCGGCTCCATCCGCAGTCGGTGGTACTACTGGAGTTGGATCGCCAAACACCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTAGTAGTTACTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATTGGGTACATCTATCAAGTGGGAACACCTACAAACCCCGTCCCTC 183
DB 136 GGGCTGGAGTGGATTGGGAGTATCTATTATAGTGGGAGCACCTACTACTAACCCGTCCTC 195
QY 184 AAGAGTCGAATTGCCATGTCGGTAGACACAGTCTGAGAACAAAGTTCTCCCTGAGGCTGAAC 243
DB 196 AAGAGTCGAGTCCCATATATCCGTAGACACGTCACAGAACACAGTTCTCCCTGAAGCTGAGC 255
QY 244 TCTGTGACTGCCGCGGACACGCGCTGTATTACTGTGCGA-----GGTTAGAT 291
DB 256 TCTGTGACCGCGCAGACACGGCTGTGTATTACTGTGCGAGGGGGAGCTACCGGGGCTAC 315
QY 292 GGCTACACTTTGGACATCTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
DB 316 TACTACGGTATGGACGTCCTGGGGCCAAAGGGACACCGGTACCGGTCTCTCTCA 366

Search completed: August 13, 2004, 07:18:06
Job time : 50.3636 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1471.46 Seconds
(without alignments)
10073.859 Million cell updates/sec

Title: US-10-027-725A-2

Perfect score: 342

Sequence: 1 ctgagctgtgccaggact.....ccctggtaaccgtctctctca 342

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_btg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rnd.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	340.4	99.5	342	9	HSA458383
2	324.4	94.9	342	9	HSA458384
3	297.2	86.9	342	9	HSA458382
4	275	80.4	432	9	HSA491911
5	273.4	79.9	432	9	HSA491912
6	271.8	79.5	354	9	HSA45064
7	271.8	79.5	414	9	AF062112
8	270.8	79.2	411	9	HST22X1
9	269	78.7	403	12	AF452917
10	268.6	78.5	351	9	HSA245020
11	268.4	78.5	351	9	HSA244930
12	268.4	78.5	358	9	AF021954
13	268.4	78.5	360	6	AX061463
14	267	78.1	360	9	HSU80129
15	267	78.1	360	9	HSU80130
16	266	77.8	354	9	HSA244955
17	265.8	77.7	400	12	AF452909
18	265.6	77.7	357	9	HSA244949
19	264.2	77.3	414	9	HST14X13
20	264.2	77.3	414	9	HST14X4
21	264	77.2	363	9	HSU80131
22	263	76.9	412	12	AF452912
23	262.8	76.8	411	9	HST14X10
24	262.4	76.7	409	12	AF452947
25	262	76.6	357	9	HSA279523
26	261.8	76.5	362	9	HSU80166
27	260.8	76.3	363	9	HSU80128
28	260.6	76.2	406	12	AF453047
29	260.4	76.1	357	9	HSA279541
30	259.6	75.9	417	9	HST14X9
31	258.8	75.7	357	9	HSA244934
32	258.8	75.7	357	9	HSA244964
33	258.8	75.7	357	9	HSA279530
34	258.8	75.7	357	9	HSA279538
35	258.8	75.7	357	9	HSU80168
36	258.4	75.6	406	12	AF453217
37	257.8	75.4	348	9	AY281334
38	257.8	75.4	366	9	HSU80111
39	257.8	75.4	369	6	AX061433
40	257.8	75.4	414	9	HST14X15
41	257.8	75.4	414	9	HST14X5
42	257.4	75.3	351	9	HSA244953
43	257.4	75.3	351	9	HSA244958
44	257.2	75.2	360	9	AB063905
45	256.6	75.0	360	9	AB067300

ALIGNMENTS

RESULT 1
LOCUS HSA458383
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 60.
ACCESSION AJ458383.1 GI:20387065
VERSION AJ458383
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Flicker S., Steinberger P., Norderhaug L., Sperr W.R., Majlesi Y., Valent P., Kraft D. and Valenta R.

Pred. No. is the number of results predicted by chance to have a

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TITLE      Conversion of grass allergen-specific human IgE into a protective
JOURNAL    IgG1 antibody
REFERENCE  2 (bases 1 to 342)
AUTHORS    Unpublished
TITLE      Flicker, S.
JOURNAL    Direct Submission
           Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
           General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
           Vienna, AUSTRIA
FEATURES   Location/Qualifiers
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            /db_xref="REMTREMBL:CAD30445"
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            Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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            Db 61 TCTGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCCAGCTCCAGGG 120
            QY 121 AAGGCCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTCTCCCTGAGACTG 180
            Db 121 AAGGCCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTCTCCCTGAGACTG 180
            QY 181 CTCAGAGTCGAATTACCATGTAGACAGTCTAAGAACCACTTCTCCCTGAGACTG 240
            Db 181 CTCAGAGTCGAATTACCATGTAGACAGTCTAAGAACCACTTCTCCCTGAGACTG 240
            QY 241 ACCTCTGTACTGCCCGGACACCGCCGCTCTATTACTGTGCGGCTCAGATGGGTACT 300
            Db 241 ACCTCTGTACTGCCCGGACACCGCCGCTCTATTACTGTGCGGCTCAGATGGGTACT 300
            QY 301 TTGGCAACTGGGGCCAGGAACCCCTGGTCACCGTCTCCTCA 342
            Db 301 TTGGCAACTGGGGCCAGGAACCCCTGGTCACCGTCTCCTCA 342
            RESULT 2
            HSA458384      342 bp mRNA linear PRI 30-APR-2002
            LOCUS      Homo sapiens partial mRNA for immunoglobulin heavy chain variable
            DEFINITION region (IGHV gene), clone 100.
            ACCESSION  AJ458384
            VERSION    AJ458384.1 GI:20387067
            KEYWORDS   IGHV gene; immunoglobulin heavy chain; variable region.
            SOURCE      Homo sapiens (human)
            ORGANISM   Homo sapiens
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                    1
                    Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,
                    Valent, P., Kraft, D. and Valenta, R.
                    Conversion of grass allergen-specific human IgE into a protective
                    IgG1 antibody
                    2 (bases 1 to 342)
                    Unpublished
                    Flicker, S.
                    Direct Submission
                    Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
                    General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
                    Vienna, AUSTRIA
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                    Db 61 TCTGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGATCCGCCAGCTCCAGGG 120
                    QY 121 AAGGCCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTCTCCCTGAGACTG 180
                    Db 121 AAGGCCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTCTCCCTGAGACTG 180
                    QY 181 CTCAGAGTCGAATTACCATGTAGACAGTCTAAGAACCACTTCTCCCTGAGACTG 240
                    Db 181 CTCAGAGTCGAATTACCATGTAGACAGTCTAAGAACCACTTCTCCCTGAGACTG 240
                    QY 241 ACCTCTGTACTGCCCGGACACCGCCGCTCTATTACTGTGCGGCTCAGATGGGTACT 300
                    Db 241 ACCTCTGTACTGCCCGGACACCGCCGCTCTATTACTGTGCGGCTCAGATGGGTACT 300
                    QY 301 TTGGCAACTGGGGCCAGGAACCCCTGGTCACCGTCTCCTCA 342
                    Db 301 TTGGCAACTGGGGCCAGGAACCCCTGGTCACCGTCTCCTCA 342
                    RESULT 3
                    HSA458382      342 bp mRNA linear PRI 30-APR-2002
                    LOCUS      Homo sapiens partial mRNA for immunoglobulin heavy chain variable
                    DEFINITION region (IGHV gene), clone 94.
                    ACCESSION  AJ458382
                    VERSION    AJ458382.1 GI:20387063
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KEYWORDS	IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y., Valent, P., Kraft, D. and Valenta, R.
TITLE	Conversion of grass allergen-specific human IgE into a protective IgG1 antibody
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 342)
AUTHORS	Flicker, S.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-2002) Flicker S., Department of Pathophysiology, General Hospital of Vienna, 30, Maehringerguertel 18-20, A-1090 Vienna, AUSTRIA
FEATURES	Location/Qualifiers
source	1..342
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gene	1..342
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CDS	<1..>342
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Query Match	86.9%; Score 297.2; DB 9; Length 342;
Best Local Similarity	91.8%; Pred. No. 7.7e-77;
Matches	314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Qy	1 CTCGAGTCTGCCAGGACTGGTAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTC 60
Db	1 CTCGAGTCTGCCAGGACTGGTAAGCCTTCACAGACCCCTGTCCCTCACTGCGCTGTC 60
Qy	61 TCTGCTGCTCCATCCGCGAGTGGTGTATTATTGGAGTTGGTCCGCCAGCCTCCAGGG 120
Db	61 TCTGCGGCTCCATCCGCGAGTGGTGTATTATTGGAGTTGGATCCGCCAACCCAGGG 120
Qy	121 AAGGCTCGGAGTGGATCGGCAACATCTATCACAGTGGCAACACTACAAACCCGCTCC 180
Db	121 AAGGCTCGGAGTGGATCGGTTACATCTATCACAGTGGCAACACTACTACACCCGCTCC 180
Qy	181 CTCAGAGTCAATTAACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240
Db	181 CTCAGAGTCAATTAACATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTG 240
Qy	241 ACCTCTGTGACTGCGCGGACACCGCGTCTATTACTGTGCGCGTCAAGATGGGTATCT 300
Db	241 AACTCTGTGACTGCGCGGACACCGCGTGTATTACTGTGCGGAGTTAGATGGCTACCT 300
Qy	301 TTGACAACTGGGCGCCAGGGAACCTGGTCAACCGTCTCCCTCA 342
Db	301 TTGACATCTGGGCGCCAGGGAACCTGGTCAACCGTCTCCCTCA 342
RESULT 4	
HSA491911	432 bp mRNA linear PRI 20-NOV-2003
LOCUS	

DEFINITION	Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region (Clone HD17 C9).
ACCESSION	AJ491911
VERSION	AJ491911.1 GI:24415808
KEYWORDS	constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 Coker, H.A., Durham, S.R. and Gould, H.J.
AUTHORS	Local somatic hypermutation and class switch recombination in the nasal mucosa of allergic rhinitis patients
TITLE	J. Immunol. 171 (10), 5602-5610 (2003)
JOURNAL	22970235
MEDLINE	14607969
REFERENCE	2 (bases 1 to 432)
AUTHORS	Coker, H.A.
TITLE	Direct Submission
JOURNAL	Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall Centre, King's College London, Guy's Campus, London, SE1 1UL, UNITED KINGDOM
FEATURES	Location/Qualifiers
source	1..432
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	/sex="female"
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CDS	<1..>432
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	/db_xref="REMBL:CAD38020"
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gene	1..355
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V_segment	1..297
	/gene="IGHV4-30"
	/note="VH segment"
D_segment	298..315
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	/note="D5-24 rf 3"
J_segment	316..355
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	/note="region JH4b"
gene	356..432
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Query Match	80.4%; Score 275; DB 9; Length 432;
Best Local Similarity	88.2%; Pred. No. 2.9e-70;

Matches 299; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 4 GAGTGTGCGCCAGGACTGGTGAAGCTTCACAGACCTGTCCCTCACTGCACTGTCTCT 63
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Db 16 GAGTGTGCGCCAGGACTGGTGAAGCTTCACAGACCTGTCCCTCACTGCACTGTCTCT 75
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QY 64 GGTGGCTCATCCGACAGTGGTGTATTATTGGAGTGGGTCCGCGAGCCTCCAGGGAAG 123
Db 76 GGTGGCGCATCAGTAGTGGTGTATTACTGGAGTGGATCCGCGAGCACCAGGGAAG 135
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QY 124 GGCCTGGAGTGATCGGCAACATCTATCATCACTGGCAACACATCAACAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGATACATCTATTACAGGGGAGCACCCTACTACAACCCGTCCTC 195
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QY 184 AAGAGTCGAATTACATGTCACTAGACAGCTTAGACACCTTCTCCCTGAGACTGACC 243
Db 196 AGGAGTCGAATAATCATGTCAATTGACAGCTGTCAAAATCAGTTCTCCCTGAGGTGACC 255
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QY 244 TCTGTGACTGCCCGGACACGCGCTCTATTACTGTGCGCGTCAAGTGGGTATCTTTG 303
Db 256 TCTGTGACTGCCCGGACACGCGCTGTATTCTGTGCGGCTAGATGGGTACAGTTTG 315
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QY 304 GACAACTGGGCGCAGGAAACCTGTGTCACCGTCTCTCTCA 342
Db 316 GACTACTGGGCGCAGGAAACCTGTGTCACCGTCTCTCTCA 354
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RESULT 5

HSA491912 432 bp mRNA linear PRI 20-NOV-2003
LOCUS Homo sapiens mRNA for immunoglobulin heavy chain V-D-J-Ce region
(clone HD17 C37).

ACCESSION AJ491912
VERSION AJ491912.1 GI:24415810
KEYWORDS constant region; epsilon chain; IGH gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Coker, H.A., Durham, S.R. and Gould, H.J.
TITLE Local somatic hypermutation and class switch recombination in the nasal mucosa of allergic rhinitis patients
J. Immunol. 171 (10), 5602-5610 (2003)
22970235
14607969

REFERENCE 2 (bases 1 to 432)
AUTHORS Coker, H.A.
TITLE Direct Submission
Submitted (26-JUN-2002) Coker H.A., Biomedical Sciences, Randall Centre, King's College London, Guy's Campus, London, SE1 1UL, UNITED KINGDOM
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="HD17 C37"
/sex="female"
/cell_type="B lymphocyte"
/tissue_type="nasal mucosa"
/dev_stage="adult"
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/country="United Kingdom"
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FEATURES

source

RESULT 6
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LOCUS Homo sapiens mRNA for immunoglobulin gamma heavy chain variable region, partial, clone 2-D123.
DEFINITION
ACCESSION AJ245064
VERSION AJ245064.1 GI:4995589
KEYWORDS IGG; Igg heavy chain; immunoglobulin gamma heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Dono, M., Zupo, S., Chiorazzi, N. and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic

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/product="immunoglobulin heavy chain variable region"
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298. .315
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356. .432
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ORIGIN

Query Match 79.9%; Score 273.4; DB 9; Length 432;
Best Local Similarity 87.9%; Pred. No. 8.6e-70;
Matches 298; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCTGTCCCTCACTGCACTGTCTCT 63
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QY 64 GGTGGCTCATCCGACAGTGGTGTATTATTGGAGTGGGTCCGCGAGCCTCCAGGGAAG 123
Db 76 GGTGGCGCATCAATAGTGGTGTATTACTGGAGTGGATCCGCGAGCACCAGGGAAG 135
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QY 124 GGCCTGGAGTGATCGGCAACATCTATCATCACTGGCAACACATCAACAACCCGTCCTC 183
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QY 184 AAGAGTCGAATTACATGTCACTAGACAGCTTAGACACCTTCTCCCTGAGACTGACC 243
Db 196 AGGAGTCGAATAATCATGTCAATTGACAGCTGTCAAAATCAGTTCTCCCTGAGGTGACC 255
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QY 244 TCTGTGACTGCCCGGACACGCGCTCTATTACTGTGCGCGTCAAGTGGGTATCTTTG 303
Db 256 TCTGTGACTGCCCGGACACGCGCTGTATTCTGTGCGGCTAGATGGGTACAGTTTG 315
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QY 304 GACAACTGGGCGCAGGAAACCTGTGTCACCGTCTCTCTCA 342
Db 316 GACTACTGGGCGCAGGAAACCTGTGTCACCGTCTCTCTCA 354
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RESULT 6

HSA245064 354 bp mRNA linear PRI 02-JUN-1999
LOCUS Homo sapiens mRNA for immunoglobulin gamma heavy chain variable region, partial, clone 2-D123.
DEFINITION
ACCESSION AJ245064
VERSION AJ245064.1 GI:4995589
KEYWORDS IGG; Igg heavy chain; immunoglobulin gamma heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Dono, M., Zupo, S., Chiorazzi, N. and Ferrarini, M.
TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	marginal zone equivalents		KEYWORDS SOURCE ORGANISM	Homo sapiens (human)		
	Unpublished			Homo sapiens		
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	Dono, M.			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	Direct Submission			1 (bases 1 to 414)		
	Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca			Wang, X. and Stollar, B.D.		
	sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova,			Immunoglobulin VH gene expression in human aging		
	ITALY			Clin. Immunol. 93 (2), 132-142 (1999)		
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	/organism="Homo sapiens"			Direct Submission		
	/mol_type="mRNA"			Submitted (22-APR-1998) Biochemistry Department, Tufts University		
	/db_xref="taxon:9606"			School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA		
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	YFYDWGGALVTVSS"			/db_xref="GI:3170687"		
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ORIGIN	KGLWIGIYYSGSTYNPISLKRVTISVDTSKNQFSLKSSVTAADTAVYVCARGIS			42; Indels		
	YFYDWGGALVTVSS"			0; Gaps		
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	YFYDWGGALVTVSS"			Query Match		
	<1. .>354			Best Local Similarity		
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	/protein_id="CAB44197.1"			42; Indels		
	/db_xref="GI:4995590"			0; Gaps		
	/db_xref="REMTREMBL:CAB44197"			0;		
	translation="QVQLQESGPGLVKPSQTLSTCTVSGGISISSADPYMNIQPPG			Query Match		
ORIGIN	KGLWIGIYYSGSTYNPISLKRVTISVDTSKNQFSLKSSVTAADTAVYVCARGIS			Best Local Similarity		
	YFYDWGGALVTVSS"			Matches		
	<1. .>354			297; Conservative		
	/gene="IGHV4-30-4"			0; Mismatches		
	/product="immunoglobulin gamma heavy chain variable			42; Indels		
	region"			0; Gaps		
	/protein_id="CAB44197.1"			0;		
	/db_xref="GI:4995590"			Query Match		
	/db_xref="REMTREMBL:CAB44197"			Best Local Similarity		
	translation="QVQLQESGPGLVKPSQTLSTCTVSGGISISSADPYMNIQPPG			Matches		
ORIGIN	KGLWIGIYYSGSTYNPISLKRVTISVDTSKNQFSLKSSVTAADTAVYVCARGIS			297; Conservative		
	YFYDWGGALVTVSS"			0; Mismatches		
	<1. .>354			42; Indels		
	/gene="IGHV4-30-4"			0; Gaps		
	/product="immunoglobulin gamma heavy chain variable			0;		
	region"			Query Match		
	/protein_id="CAB44197.1"			Best Local Similarity		
	/db_xref="GI:4995590"			Matches		
	/db_xref="REMTREMBL:CAB44197"			297; Conservative		
	translation="QVQLQESGPGLVKPSQTLSTCTVSGGISISSADPYMNIQPPG			0; Mismatches		
ORIGIN	KGLWIGIYYSGSTYNPISLKRVTISVDTSKNQFSLKSSVTAADTAVYVCARGIS			42; Indels		

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RESULT 8
LOCUS HST22X1 411 bp mRNA linear PRI 30-APR-1997
DEFINITION H sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone T22.1).
ACCESSION Z75385.1 GI:2062048
VERSION 1
KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS Tonnelie,C., D'Ercole,C., Depraetere,V., Metras,D., Boubli,L. and Fougereau,M.
TITLE Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?
JOURNAL Int. Immunol. 9 (3), 407-414 (1997)
MEDLINE 97244170
PUBMED 9089979
REFERENCE 2 (bases 1 to 411)
AUTHORS Tonnelie,C.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-1996) Cecile Tonnelie, Centre d'Immunologie Marseille Luminy, Marseille, 13288, France
FEATURES
source
1..411
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="T22.1"
/cell_type="B-lymphocyte"
/tissue_type="thymus"
/clone_lib="T22"
/dev_stage="infant"
V_region
1..411
/product="Ig heavy chain variable region (VH4DJ)"
sig_peptide
1..57
V_segment
58..354
D_segment
355..377
J_segment
378..411
ORIGIN
Query Match 79.2%; Score 270.8; DB 9; Length 411;
Best Local Similarity 87.6%; Pred. No. 5.1e-69; Mismatches 42; Indels 0; Gaps 0;
Matches 296; Conservative 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCCTCACCCTGCACCTGTCTCT 63
DB 73 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCCTCACCCTGCACCTGTCTCT 132
QY 64 GTTGGCTCATCCGACGTGGTGGTTATTATTGGAGTTGGGTGGCGGAGCCTCCAGGGAAG 123
DB 133 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGGCTGCACCCAGGAAG 192
QY 124 GGCCTGGAGTGGTGGCAACATCTATCAGTGGCAACACCTACACCAACCGTCCCTC 183
DB 193 GGCCTGGAGTGGGTGGTACATCTATTACGTGGGAGCACCTACTACACCCGTCCTC 252
QY 184 AAGAGTCGAATTAACATGTCACTAGACAGCTTAAGAACAACCTTCTCCCTGAGACTGACC 243
DB 253 AAGAGTCGAGTTACCATATCAGTAGACAGCCCTAAGAACCAGTTCTCCCTGAAGCTGAGC 312
QY 244 TCTGTGACTGCGCGGACAGCGCCCTCTATTACTGTGGCGGTGACATGGGTATCTTTG 303
DB 313 TCTGTGACTGCGCGGACAGCGCCGTGTTACTGTGGAGAGTGGGTTATTGTGTAGTAGT 372
QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTC 341
DB 373 TCCAGTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTC 410
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```
RESULT 9
LOCUS AF452917 403 bp mRNA linear SYN 01-DEC-2002
DEFINITION Synthetic construct clone 7-161VH rotavirus VP7-specific antibody heavy chain variable region mRNA, partial sequence.
ACCESSION AF452917
VERSION 1
KEYWORDS AF452917.1 GI:25988060
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 403)
AUTHORS Weitkamp,J.-H. and Crowe,J.E. Jr.
TITLE Infant B Cell Repertoires are Sufficiently Diversified for Mature Virus-Specific Responses, but Lack Somatic Mutations
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 403)
AUTHORS Weitkamp,J.-H. and Crowe,J.E. Jr.
TITLE Direct Submission
JOURNAL Submitted (28-NOV-2001) Pediatrics, Vanderbilt University Medical Center, 1161 21st Avenue South, D-7235 Medical Center North, Nashville, TN 37232-2581, USA
FEATURES
source
1..403
Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/clone="7-161VH"
/note="includes synthetic primer used to amplify the sequence from Homo sapiens mRNA"
misc_feature
1..>403
/note="rotavirus VP7-specific antibody heavy chain variable region"
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ORIGIN

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Query Match 78.7%; Score 269; DB 12; Length 403;
Best Local Similarity 88.9%; Pred. No. 1.7e-68;
Matches 303; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 5 AGTCGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCCTCACCCTGCACCTGTCTCTG 64
DB 42 AGTCGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCCTCACCCTGCACCTGTCTCTG 101
QY 65 GTGGCTCCATCGCAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGAAGG 124
DB 102 GTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCGCCAGCACCCAGGAAGG 161
QY 125 GCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTACCAACCCCGTCCCTCA 184
DB 162 GCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTTACTACACCCGTCCCTCA 221
QY 185 AGAGTCGAATTAACCATGTCTAGTAGACAGCTTAAGAACCACCTTCTCCCTGAGACTGACCT 244
DB 222 AGAGTCGAATTAACCATATCAGTAGACAGCTTAAGAACCAGTCTCCCTGAAAGCTGAGCT 281
QY 245 CTGTCACTGCCGCGACACGCGCTTATTACTGTGGG---CGGTCAAGATGGGTATACCT 301
DB 282 CTGTCACTGCCGCGACACGCGCTGTATTACTGTGGGAGAGGTGGGTACGGCTGACT 341
QY 302 TGGACAACATGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
DB 342 TTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 382
```

```
RESULT 10
LOCUS HSA245020 351 bp mRNA linear PRI 01-JUN-2000
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone 2-E66.
ACCESSION AJ245020
VERSION AJ245020.1 GI:4995498
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KEYWORDS IGM; IgM heavy chain; immunoglobulin mu heavy chain; variable region

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)

MEDLINE 20281644

PUBMED 10820234

REFERENCE 2 (bases 1 to 351)

AUTHORS Dono, M.

TITLE Direct Submission

JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

FEATURES

source Location/Qualifiers

1..351

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/chromosome="14"

/clone="2-E66"

/cell_type="B-lymphocyte"

/tissue_type="tonsil"

/rearranged

1..351

/gene="IGHV4-30-4"

<1..>351

/gene="IGHV4-30-4"

/codon_start=1

/product="immunoglobulin mu heavy chain variable region"

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/db_xref="GI:4995499"

/db_xref="REMTREMBL:CAB44154"

/translation="QVQLQESGPGLVKPSQTLSTCTVSGSISGGYYSWIRQPPGKGLEWIGIYYISGTYNPSLKRVTISVDTSKNQFSLKLSVTAADTAVYVCARGWSDYWGQGDTLVTS"

<1..>351

/gene="IGHV4-30-4"

/product="immunoglobulin mu heavy chain variable region"

ORIGIN

Query Match 78.5%; Score 268.6; DB 9; Length 351;

Best Local Similarity 89.1%; Pred. No. 2.2e-68;

Matches 302; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 63

Db 16 GAGTCGGGCCCAGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 75

QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123

Db 76 GGTGGCTCCATCAGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 135

QY 124 GGCTTGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTACCAACCCGTCCTC 183

Db 136 GGCTTGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTACCAACCCGTCCTC 195

QY 184 AAGAGTCAATTACATGTCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGCTGACC 243

Db 196 AAGAGTCAATTACATGTCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGCTGACC 255

QY 244 TCTGTAGTCCGCGGACACGCGCTCTATTACTGTGCGCGGTGAGTGGTATCTTG 303

Db 256 TCTGTAGTCCGCGGACACGCGCTCTATTACTGTGCGCGGTGAGTGGTATCTTG 312

QY 304 GACAACTGGGGCCAGGGAACCTGGTCAACCCGTCCTCA 342

Db 313 GACTACTGGGCCAGGGAACCTGGTCAACCGTCTCTCA 351

RESULT 11

HSA244930 351 bp mRNA linear PRI 01-JUN-2000

LOCUS HSA244930

DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone 1-A34.

ACCESSION AJ244930

VERSION AJ244930.1 GI:4995319

KEYWORDS IGM; IgM heavy chain; immunoglobulin mu heavy chain; variable region.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.

TITLE Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents

JOURNAL J. Immunol. 164 (11), 5596-5604 (2000)

MEDLINE 20281644

PUBMED 10820234

REFERENCE 2 (bases 1 to 351)

AUTHORS Dono, M.

TITLE Direct Submission

JOURNAL Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna Benzi 10- Genova, ITALY

FEATURES

source Location/Qualifiers

1..351

/organism="Homo sapiens"

/mol_type="mRNA"

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/chromosome="14"

/clone="1-A34"

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/tissue_type="tonsil"

/rearranged

1..351

/gene="IGHV4-31"

<1..>351

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/codon_start=1

/product="immunoglobulin mu heavy chain variable region"

/protein_id="CAB44065.1"

/db_xref="GI:4995320"

/db_xref="REMTREMBL:CAB44065"

/translation="QLQESGPGLVKPSQTLSTCTVSGSISGGYYSWIRQHPGKLEWIGIYYISGTYNPSLKRVTISVDTSKNQFSLKLSVTAADTAVYVCARGKDFYFDYWGQGDTLVTS"

<1..>351

/gene="IGHV4-31"

/product="immunoglobulin mu heavy chain variable region"

ORIGIN

Query Match 78.5%; Score 268.4; DB 9; Length 351;

Best Local Similarity 88.6%; Pred. No. 2.6e-68;

Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCCAGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 63

Db 10 GAGTCGGGCCCAGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 69

QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123

Db 70 GGTGGCTCCATCAGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 129

QY 124 GGCTTGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTACCAACCCGTCCTC 183

Db 130 GGCTTGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTACCAACCCGTCCTC 189

QY 184 AAGAGTCGAATTACCATGTCTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
 |||||
 Db 190 AAGAGTCGAGTTACCATATCACTAGACACGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 249
 |||||
 QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGGG---CGGTGAGATGGGTATCT 300
 |||||
 Db 250 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGAGGCAAGAGAGACTTCTAC 309
 |||||
 QY 301 TTGGACAACTGGGCGGAGGACCTGTGTCACCGTCTCTCTCA 342
 |||||
 Db 310 TTGACTACTGGGCGGAGGAAACCTGTGTCACCGTCTCTCTCA 351
 |||||

RESULT 12
 AF021954
 LOCUS Homo sapiens ID:CLL019 IgM heavy chain variable region mRNA, 358 bp mRNA linear PRI 02-APR-1998
 DEFINITION partial cds.
 ACCESSION AF021954
 VERSION AF021954.1 GI:3004697
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE Differences in Ig variable region gene use and mutation in IgM vs IgG CLL suggest selection for distinct surface membrane Ig receptors

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 358)
 AUTHORS Chiorazzi, N.
 TITLE Direct Submission

JOURNAL Submitted (02-SEP-1997) Medicine, North Shore University Hospital, 350 Community Drive, Manhasset, NY 11030, USA
 LOCATION/Qualifiers

FEATURES
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 1..358
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /chromosome="14"
 /clone="ID:CLL019"
 /cell_type="B lymphocyte"
 <1..358
 /codon_start=1
 /product="IgM heavy chain variable region"
 /protein_id="AAC09088.1"
 /db_xref="GI:3004698"
 /translation="QVQLQESGFLVKPSQTLSTLTCTVSGGSISSGGYVWSWIRHPG KGLEWIGYIYSGSYNPNLSKSRVTISVDTSKNQFSLKLSVTAADTAIVYCAKGAT VTHFDYWGQGLVTVSS"
 CDS

ORIGIN

Query Match 78.5%; Score 268.4; DB 9; Length 358;
 Best Local Similarity 88.6%; Pred. No. 2.6e-68;
 Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCTGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 63
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 Db 16 GAGTCTGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 75
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QY 64 GTTGGCTCCATCCGCACTGTGTTATTATTGGAGTTGGGTCCGCGAGCTCCAGGGAAG 123
 |||||
 Db 76 GTTGGCTCCATCAGCACTGTGTTACTACTGGAGCTGGATCCGCGAGCACCCAGGGAAG 135
 |||||

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTTC 183
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 Db 136 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTTC 195
 |||||

QY 184 AAGAGTCGAATTACCATGTCTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
 |||||
 Db 196 AAGAGTCGAGTTACCATATCACTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGAGC 255
 |||||

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGGCGGTCTAGATGGGTATAC---T 300
 |||||
 Db 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTCAAGAGGAGCTACGCTGACCCAC 315
 |||||
 QY 301 TTGGACAACTGGGCGGACGGAACCTGTGTCACCGTCTCTCTCA 342
 |||||
 Db 316 TTGACTACTGGGCGGAGGAAACCTGTGTCACCGTCTCTCTCA 357
 |||||

RESULT 13
 AX061463
 LOCUS Sequence 32 from Patent WO0100678. 360 bp DNA linear PAT 22-JAN-2001
 DEFINITION
 ACCESSION AX061463
 VERSION AX061463.1 GI:12406598

KEYWORDS
 SOURCE Human immunodeficiency virus 1 (HIV-1)
 ORGANISM Human immunodeficiency virus 1
 Viruses; Retroviridae; Lentivirus; Primate
 lentivirus group.

REFERENCE
 AUTHORS Watkins, B.A. and Reitz, M.S.
 TITLE Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120
 JOURNAL Patent: WO 0100678-A 32 04-JAN-2001;
 THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)

FEATURES
 source
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 /organism="Human immunodeficiency virus 1"
 /mol_type="unassigned DNA"
 /db_xref="taxon:11676"
 /note="VH"

ORIGIN

Query Match 78.5%; Score 268.4; DB 6; Length 360;
 Best Local Similarity 88.6%; Pred. No. 2.6e-68;
 Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCTGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 63
 |||||
 Db 19 GAGTCTGCGCCAGGACTGTGAGCCTTCACAGACCTCTCCCTCACCTGCACTGTCTCT 78
 |||||

QY 64 GTTGGCTCCATCCGCACTGTGTTATTATTGGAGTTGGGTCCGCGAGCTCCAGGGAAG 123
 |||||
 Db 79 GTTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCGAGCACCCAGGGAAG 138
 |||||

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTTC 183
 |||||
 Db 139 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTTC 198
 |||||

QY 184 AAGAGTCGAATTACCATGTCTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
 |||||
 Db 199 AAGAGTCGAGTTACCATATCACTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGAGC 258
 |||||

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGG---CGGTGAGATGGGTATCT 300
 |||||
 Db 259 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAGAGGGGTAGTAGGACTGG 318
 |||||

QY 301 TTGGACAACTGGGCGGAGGAAACCTGTGTCACCGTCTCTCTCA 342
 |||||
 Db 319 TTCGACCCCTGGGCGGAGGAAACCTGTGTCACCGTCTCTCTCA 360
 |||||

RESULT 14
 HSU80129
 LOCUS Human immunoglobulin heavy chain variable region (V4-31) gene, partial cds. 360 bp DNA linear PRI 19-FEB-1997
 DEFINITION
 ACCESSION U80129
 VERSION U80129.1 GI:1791100

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

1 (bases 1 to 360)
Glas,A.M., Nottenburg,C. and Milner,E.C.
Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
Clin. Exp. Immunol. 107 (2), 372-380 (1997)
97182739
9030878
2 (bases 1 to 360)
Glas,A.M., Nottenburg,C. and Milner,E.C.B.
Direct Submission
Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
Location/Qualifiers
1. .360
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/mol_type="genomic DNA"
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/chromosome="14"
/map="14q32-q33"
/clone="3f1c2"
/cell_type="CD19+ B cells"
/tissue_type="peripheral blood"
/note="CD19+ peripheral blood B cells obtained from a bone
marrow transplant recipient 1 year post transplant; clone
54 in reference 1"
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/product="immunoglobulin heavy chain variable region"
/protein_id="AAC51044.1"
/db_xref="GI:1791101"
/translation="OVQLOPSGRLVKPSQTLSTCTVSGSISGGYVWSWIRQHPG
KGLEWIGYIYSGSYNPSLKSRTVISVTSKNQPSLKLSSVTAADTAVYICARGVS
GWYFYDWGGTLLVTSS"

gene

CDS

ORIGIN

Query Match 78.1%; Score 267; DB 9; Length 360;
Best Local Similarity 88.1%; Pred. No. 6.7e-68;
Matches 304; Conservative 0; Mismatches 35; Indels 6; Gaps 1;

QY 4 GAGTCTGCCAGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGACTGTCTCT 63
DB 16 GAGTCGGGCCAGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGACTGTCTCT 75

QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTGGTGGTGTATTCTGGAGCTGGATCCGCCAGCACCAGGGAAG 135

QY 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACACAAACCCGTCCTC 183
DB 136 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGGAGCACCTACTACACCCGTCCTC 195

QY 184 AAGAGTCGAATTACCATGTGATAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAGTTACCATGTGATAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGAGC 255

QY 244 TCTGTGACTGCCGGGACACGGCCGTCTATTACTGTGGGG-----GTCCAGTGGGTAT 297
DB 256 TCTGTGACTGCCGGGACACGGCCGTCTATTACTGTGGAGAGGGGTGAGTGGGTGGTAC 315

QY 298 ACTTTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 342
DB 316 TATTTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 360

RESULT 15

HSU80130

LOCUS

HSU80130 360 bp DNA linear PRI 19-FEB-1997

DEFINITION Human immunoglobulin heavy chain variable region (V4-31) gene,
partial cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

U80130
U80130.1 GI:1791102
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Glas,A.M., Nottenburg,C. and Milner,E.C.
Analysis of rearranged immunoglobulin heavy chain variable region
genes obtained from a bone marrow transplant (BMT) recipient
Clin. Exp. Immunol. 107 (2), 372-380 (1997)
97182739
9030878
2 (bases 1 to 360)
Glas,A.M., Nottenburg,C. and Milner,E.C.B.
Direct Submission
Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
Location/Qualifiers
1. .360
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q32-q33"
/clone="3f1e2"
/cell_type="CD19+ B cells"
/tissue_type="peripheral blood"
/note="CD19+ peripheral blood B cells obtained from a bone
marrow transplant recipient 1 year post transplant; clone
55 in reference 1"
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/gene="V4-31"
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/note="Ig VH4 heavy chain"
/codon_start=1
/product="immunoglobulin heavy chain variable region"
/protein_id="AAC51045.1"
/db_xref="GI:1791103"
/translation="QVQLOPSGRLVKPSQTLSTCTVSGSISGGYVWSWIRQHPG
KGLEWIGYIYSGSYNPSLKSRTVISVTSKNQPSLKLSSVTAADTAVYICARGVS
GWYFYDWGGTLLVTSS"

gene

CDS

ORIGIN

Query Match 78.1%; Score 267; DB 9; Length 360;
Best Local Similarity 88.1%; Pred. No. 6.7e-68;
Matches 304; Conservative 0; Mismatches 35; Indels 6; Gaps 1;

QY 4 GAGTCTGCCAGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGACTGTCTCT 63
DB 16 GAGTCGGGCCAGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGACTGTCTCT 75

QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTGGTGGTGTATTCTGGAGCTGGATCCGCCAGCACCAGGGAAG 135

QY 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACACAAACCCGTCCTC 183
DB 136 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGGAGCACCTACTACACCCGTCCTC 195

QY 184 AAGAGTCGAATTACCATGTGATAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAGTTACCATGTGATAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGAGC 255

QY 244 TCTGTGACTGCCGGGACACGGCCGTCTATTACTGTGGGG-----GTCCAGTGGGTAT 297
DB 256 TCTGTGACTGCCGGGACACGGCCGTCTATTACTGTGGAGAGGGGTGAGTGGGTGGTAC 315

QY 298 ACTTTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 342

Db 316 TATTTGACTACTGGGGCCAGGGAAACCCCTGGTTCACCGTCTCCTCA 360

Search completed: August 13, 2004, 03:57:59
Job time : 1472.46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 2005.71 Seconds
(without alignments)
5091.898 Million cell updates/sec

Title: US-10-027-725A-2

Perfect score: 342

Sequence: 1 ctcgagctgcggccaggact.....ccctgggtcacggtctctctca 342

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	263.8	77.1	832	9	AUI22174
2	250.8	73.3	509	10	AW406349
3	250.2	73.2	369	10	AW404242
4	250.2	73.2	677	12	BG686767

5	249.6	73.0	607	12	BM783015
6	248.2	72.6	490	14	CD689564
7	241.4	70.6	725	12	BG431274
8	241.2	70.5	643	9	AUI34293
9	240	70.2	904	13	BQ710488
10	239.8	70.1	959	13	BU899307
11	238.8	69.8	890	13	EX324929
12	238.2	69.6	903	13	BQ706579
13	238.2	69.6	1108	12	BM920469
14	237.2	69.4	977	13	EX336901
15	237.2	69.4	1201	13	EX336959
16	237	69.3	914	12	BG757054
17	237	69.3	939	13	BQ708070
18	236.4	69.1	828	10	BF974568
19	236.2	69.1	1050	9	AL552672
20	235.2	68.8	447	10	AW402200
21	234.8	68.7	596	12	BM817833
22	234.8	68.7	813	13	BQ710364
23	234.6	68.6	582	10	AW401348
24	234.6	68.6	814	12	BG685325
25	233.6	68.3	1019	13	BQ072420
26	233.6	68.3	1195	13	BQ707644
27	233.4	68.2	474	10	AW408410
28	233.4	68.2	915	13	BQ706358
29	233.2	68.2	658	13	EX505812
30	233	68.1	1201	13	EX380759
31	232.8	68.1	421	10	AW407630
32	232	67.8	363	10	AW403420
33	232	67.8	915	13	BQ711871
34	232	67.8	923	13	BQ707945
35	232	67.8	928	13	BQ707875
36	232	67.8	959	13	BQ709473
37	231.8	67.8	924	13	BQ708516
38	231.6	67.7	924	12	BG758027
39	231.6	67.7	987	13	BQ707970
40	231.4	67.7	650	12	BG684403
41	231.4	67.7	778	10	BF975836
42	231.4	67.7	929	12	BG341823
43	231	67.5	524	13	BU429270
44	231	67.5	856	13	BQ421299
45	230.6	67.4	661	12	BG686421

ALIGNMENTS

RESULT 1

AUI22174

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AUI22174 MAMMAL Homo sapiens cDNA clone MAMMAL001802 5', mRNA
832 bp linear EST 01-AUG-2002

sequence.

AUI22174

AUI22174.1 GI:10937409

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 832)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

HRI human cDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

source
1..832
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MAMMAL001802"
/tissue_type="mammary gland"
/clone_lib="MAMMAL"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 77.1%; Score 263.8; DB 9; Length 832;
Best Local Similarity 86.1%; Pred. No. 5.8e-58;
Matches 292; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 63
DB 110 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 169

QY 64 GTGGCTCCATCCGACGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 123
DB 170 GTGGCTCCATCCGACGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 229

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACACCCGTCCTCTC 183
DB 230 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACACCCGTCCTCTC 289

QY 184 AAGAGTCGAATTACCATGTCTAGTACACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 290 AAGAGTCGAATTACCATGTCTAGTACACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 349

QY 244 TCTGTGACTGCGCGGACACCGCGTCTATTACTGTGGCGGTCTAGTGGGTATCTTTG 303
DB 350 TCTGTGACTGCGCGGACACCGCGTCTATTACTGTGGCGGTCTAGTGGGTATCTTTG 409

QY 304 GACAACTGGGGCCAGGAAACCTTGTCTACCGTCTCTCTCA 342
DB 410 GACTTCTGGGGCCAGGAAACCTTGTCTACCGTCTCTCTCA 448

RESULT 2
AW406349
LOCUS
DEFINITION
UI-HF-BL0-aco-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens linear EST 16-FEB-2000
IMAGE:3059933 5', mRNA sequence.

ACCESSION
AW406349
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES

source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:3059933"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb), directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 73.3%; Score 250.8; DB 10; Length 509;
Best Local Similarity 85.4%; Pred. No. 1.1e-54;
Matches 292; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 63
DB 54 GAGTGGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCACCTGCACCTGTCTCT 113

QY 64 GTGGCTCCATCCGACGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 123
DB 114 GTGGCTCCATCCGACGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTCACCTGCACCTGTCTCT 173

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACACCCGTCCTCTC 183
DB 174 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACACCCGTCCTCTC 233

QY 184 AAGAGTCGAATTACCATGTCTAGTACACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 234 AAGAGTCGAATTACCATGTCTAGTACACAGTCTAAGAACCACTTCTCCCTGAGACTGACC 293

QY 244 TCTGTGACTGCGCGGACACCGCGTCTATTACTGTGGCGGTCTAGTGGGTATCTTTG 300
DB 294 TCTGTGACTGCGCGGACACCGCGTCTATTACTGTGGCGGTCTAGTGGGTATCTTTG 353

QY 301 TTGGACAACTGGGGCCAGGAAACCTTGTCTACCGTCTCTCTCA 342
DB 354 TTGGACAACTGGGGCCAGGAAACCTTGTCTACCGTCTCTCTCA 395

RESULT 3

AW404242
LOCUS
DEFINITION
UI-HF-BL0-abg-f-09-0-UI.r1 NIH_MGC_37 Homo sapiens linear EST 16-FEB-2000
IMAGE:3057545 5', mRNA sequence.

ACCESSION
AW404242
VERSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 369)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source
1..369
Location/Qualifiers
/organism="Homo sapiens"


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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3057545"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/clone_lib="DH10B (LTI)"
/notes="Vector: pMT3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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ORIGIN

```

Query Match      73.2%; Score 250.2; DB 10; Length 369;
Best Local Similarity 86.5%; Pred. No. 1.4e-54;
Matches 276; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy  4  GAGTCTGCGCCAGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGCACTGTCTCT 63
    |||||
Db  34  GAGTCTGCGCCAGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGCACTGTCTCT 93
    |||||

Qy  64  GGTGGCTCCATCCGACAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
    |||||
Db  94  GGTGGCTCCATCAGCAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 153
    |||||

Qy  124  GGCTGAGTGGATCGGCAACATCTATCAGTGGCAACACTACACAAACCCGTCCTC 183
    |||||
Db  154  GGCTGAGTGGATCGGCAACATCTATCAGTGGCAACACTACACAAACCCGTCCTC 213
    |||||

Qy  184  AAGAGTGGATACCATGTCTAGTAGACGCTTAAGACCACTCTCCCTGAGACTGACC 243
    |||||
Db  214  AAGAGTGGATACCATGTCTAGTAGACGCTTAAGACCACTCTCCCTGAGACTGACC 273
    |||||

Qy  244  TCTGTGACTGCGCGGACACGGCGCTTATTACTGTGCGCGGTGAGATGGTATCTTTG 303
    |||||
Db  274  TCTGTGACTGCGCGGACACGGCGGTATATTACTGTGCGGAGATCTTTGGGTATCTTT 333
    |||||

Qy  304  GACAACTGGGCGCCAGGGA 322
    |||||
Db  334  GATAGTAGTGGTTACGGAA 352
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```

```

RESULT 4
LOCUS      BG686767
DEFINITION 602650737F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763217 5',
            mRNA sequence.
ACCESSION  BG686767
VERSION     BG686767.1  GI:13918164
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 677)
REFERENCE   NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
JOURNAL     Contact: Robert Strausberg, Ph.D.
COMMENT     Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LCM1618 row: i column: 10
            High quality sequence stop: 675.
FEATURES    Location/Qualifiers
            1..677
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4763217"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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ORIGIN
Query Match      73.2%; Score 250.2; DB 12; Length 677;
Best Local Similarity 87.0%; Pred. No. 1.8e-54;
Matches 300; Conservative 0; Mismatches 38; Indels 7; Gaps 2;

Qy  4  GAGTCTGCGCCAGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGCACTGTCTCT 63
    |||||
Db  99  GAGTCTGCGCCAGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGCACTGTCTCT 158
    |||||

Qy  64  GTGGCTCCATCCGACAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
    |||||
Db  159  GTGGCTCCATCCGACAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 217
    |||||

Qy  124  GGCTGAGTGGATCGGCAACATCTATCAGTGGCAACACTACACAAACCCGTCCTC 183
    |||||
Db  218  GGCTGAGTGGATCGGCAACATCTATCAGTGGCAACACTACACAAACCCGTCCTC 277
    |||||

Qy  184  AAGAGTGGATACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
    |||||
Db  278  AAGAGTGGATACCATGTCTAGTAGACGCTTAAGAACCACTTCTCCCTGAGACTGACC 337
    |||||

Qy  244  TCTGTGACTGCGCGGACACGGCGCTTATTACTGTGCGG-----CGTCAGATGGGTAT 297
    |||||
Db  338  TCTGTGACTGCGCGGACACGGCGCTTATTACTGTGCGGAGATCGCAAGAGAGAGGC 397
    |||||

Qy  298  ACTTTGGACAACCTGGGCGCAGGGAACCTGTGTCACCGTCTCCTCA 342
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Db  398  GGGTTTCAGCCCTGGGCGCAGGGAACCTGTGTCACCGTCTCCTCA 442
    |||||

```

```

RESULT 5
LOCUS      BM783015
DEFINITION K-EST0060735 S18N669761 Homo sapiens cDNA clone S18N669761-2-E06
            5', mRNA sequence.
ACCESSION  BM783015
VERSION     BM783015.1  GI:19131247
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 607)
REFERENCE   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
            21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 2 row: E column: 06

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High quality sequence stop: 607.

FEATURES
source

1..607
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S18N669761-2-E06"
/sex="F"
/lab_host="Top10F"
/clone_lib="S18N669761"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 73.0%; Score 249.6; DB 12; Length 607;
Best Local Similarity 84.8%; Pred. No. 2.5e-54;
Matches 295; Conservative 0; Mismatches 44; Indels 9; Gaps 1;

QY 4 GAGTGTGCGCCAGGACTGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTCTCTCT 63
Db 112 GAGTGTGCGCCAGGACTGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTCTCTCT 171
QY 64 GGTGGCTCCATCCGCGAGTGGTGGTTATTATTGGAGTTGGGTCGGCCAGCCTCCAGGGAAG 123
Db 172 GGTGGCTCCATGAACAGTGGTAGTTACTACTGGAGTGGATCGGCCAACACCCAGGGAAG 231
QY 124 GGCCTGGAGTGTGCGCAACATCTATCAGTGGCAACCTTACAGAACCCGTCCTC 183
Db 232 GGCCTGGAGTGGTGGTACATCTATCAGTGGGAGCACCTTACTAGAACCCGTCCTC 291
QY 184 AAGAGTCGAATTACCATGTCACTAGACAGCTTAAGAACCACTTCTCCTGAGAGTGAAC 243
Db 292 AAGAGTCGAATTACCATGTCACTAGACAGCTTAAGAACCACTTCTCCTGAGAGTGAAC 351
QY 244 TCTGTGACTGCGCGGACACCGCCGTCTATTACTGTGCGG-----GTGAGATGGG 294
Db 352 TCTGTGACTGCGCGGACACCGCCGTCTATTACTGTGCGAGAGTGGCAATTACGATATT 411
QY 295 TATAGTTTGGACAACTGGGCGCAGGAAACCTTGTTCACCGTCTCTCA 342
Db 412 TACGGTATGGAGCTGTGGGCGCAGGAGCACCGGTCAACCGTCTCTCTCA 459

RESULT 6
CD689564
LOCUS
DEFINITION EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD689564
VERSION CD689564.1 GI:32209443
KEYWORDS EST.
SOURCE
Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 490)
AUTHORS Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)

COMMENT

Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES
source

1..490
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from Southern Chinese"

ORIGIN

Query Match 72.6%; Score 248.2; DB 14; Length 490;
Best Local Similarity 85.0%; Pred. No. 5.3e-54;
Matches 290; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 5 AGTCTGGCCGAGGACTGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTCTCTG 64
Db 111 AGTCTGGCCGAGGACTGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTCTCTG 170
QY 65 GTGGCTCCATCCGCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 124
Db 171 GTGGCTCCATCCGCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 230
QY 125 GCTTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTACAAACCCGTCCTCA 184
Db 231 GCCTGAGTGGATTGGGTACATCTATCAGTGGGAGTGGCGACTACACCCGTCCTCA 290
QY 185 AGAGTCGAATTACCATGTCACTAGACAGCTTAAGAACCACTTCTCCTGAGAGTGAAC 244
Db 291 AGAGTCGAATTACCATGTCACTAGACAGCTTAAGAACCACTTCTCCTGAGTGAAGT 350
QY 245 CTGTGACTGCGCGGACACCGCCGTCTATTACTGTGCGGCTCAGAT---GGGTACTCT 301
Db 351 CTGTGACGCGCGGACACCGCCGTCTATTACTGTGCGAGAAATGGGTCCCGAGCAGTAA 410
QY 302 TGGCAACTGGGGCCAGGGAACCCCTGTGTCACCGTCTCTCTCA 342
Db 411 TTGACTACTGGGGCCAGGGAATCCTGGTCACCGTCTCTCTCA 451

RESULT 7
BG431274

LOCUS BG431274 725 bp mRNA linear EST 14-MAR-2001
DEFINITION 602499844F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613435 5', mRNA sequence.

ACCESSION BG431274
VERSION BG431274.1 GI:13337780
KEYWORDS EST.
SOURCE
Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 725)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Plate: LLCM1363 row: h column: 12

High quality sequence stop: 716.

FEATURES

source
1. .725
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4613435"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH_MGC_75"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATCTAGAGCCGGGGGGGGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.6%; Score 241.4; DB 12; Length 725;
Best Local Similarity 82.0%; Pred. No. 3.7e-52;
Matches 278; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 4 GAGTCTGCGCCAGACACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGACTGTCTCT 63
Db |||||
109 GAGTGGGGCCCAAGACTGGTGAAGCCTTCGCGGGACCTGTCCCTCAGCTGACTGTCTCT 168
QY 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGGTCCGCCACCTCCAGGGAAG 123
Db |||||
169 GGTGGCTCCATCATCATGTCCTCCATTTATTCTGGGGCTGGATCCGCCAGCCCGCAGGGAAG 228
QY 124 GGCCTGAGTGGATCGGCAACATCTACAGTGGGCAACCTTACACAAACCCGTCCTC 183
Db |||||
229 GGGCTGGAGTGGATTGCGAGTATCTCTCACAGTGGGACCACTACTCAACCCGTCCTC 288
QY 184 AAGAGTCGATTAACCATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db |||||
289 GAGAGTCGAGTCAACCATATCGTAGACAGCTCCAGAACCACTTCTCCCTGAGCTGAGG 348
QY 244 TCTGTGACTGCGGGGACAGCGCGTCTATTACTGTGCGGGTCCAGATGGGTATCTTTG 303
Db |||||
349 CCTGTGACCGCCGAGACAGCTCTGTATATTATTGCGGAGATTCTCGGGGGAGTTT 408
QY 304 GACAATGGGGCCAGGAAACCTGGTCAACCTGTCTCTCA 342
Db |||||
409 GACTATTGGGGCCAGGAAACCTGGTCCGCTCTCTCA 447

RESULT 8

AUI34293
LOCUS AUI34293 OVARC1 Homo sapiens cDNA clone OVARC1001672 5', mRNA
DEFINITION AUI34293 643 bp linear EST 01-AUG-2002
sequence.
ACCESSION AUI34293
VERSION AUI34293.1 GI:10994832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 643)
AUTHORS Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
CONTACT: Takao Isogai
COMMENT Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp
HRI human cDNA project; 5' & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

source
1. .643
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="OVARC1001672"
/tissue_type="ovary, tumor tissue"
/clone_lib="OVARC1"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 70.5%; Score 241.2; DB 9; Length 643;
Best Local Similarity 82.9%; Pred. No. 4e-52;
Matches 295; Conservative 0; Mismatches 43; Indels 18; Gaps 1;

QY 5 AGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGACTGTCTCTG 64
Db |||||
110 AGTGGGCCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGACTGTCTCTG 169
QY 65 GTGGCTCATCCGACGTGGTGGTATTATTGGAGTTGGGTCCGCCACCTCCAGGGAAG 124
Db |||||
170 GTGGCTCATCAGCAGTGGTGAATTCTTGGACCTGGATCCGCCAACACCCAGGGAAG 229
QY 125 GCTGGAGTGGATCGGCAACATCTATCAGACCTGGCAGCAGCTACACAAACCCGTCCTCA 184
Db |||||
230 GCCTTGGAGTGGATGGGTATCTATTACAGTGGGACCACTACTACAAACCCGTCCTCA 289
QY 185 AGAGTCGAATTACCATGTCTAGTAGACACAGCTCTAAGAACCACTTCTCCCTGAGACTGACCT 244
Db |||||
290 AGAGTCGAGTTACCATATCAATAGACACAGCTAAGAACCACTTCTCCCTGAGCTGAGCG 349
QY 245 CTGTGACTGCGGGGACACGCGCGTCTATTACTGTGCGGGTCCAGATGGGTATCTACT --- 300
Db |||||
350 CTGTGACTGCGGGGACACGCGCGTCTATTACTGTGCGAGTTTGTAGACCTTTAATAGTG 409
QY 301 -----TTGGCAACTGGGGCCAGGAAACCTGGTCCGCTCTCTCA 342
Db |||||
410 GGACCTACAGTAAGTTTGACCACTGGGGCCAGGAAACCTGGTCCGCTCTCTCA 465

RESULT 9

BQ710488
LOCUS BQ710488 904 bp mRNA linear EST 16-JUL-2002
DEFINITION BQ710488 9352970 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278137
5', mRNA sequence.
ACCESSION BQ710488
VERSION BQ710488.1 GI:21849387
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 904)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNC2465 row: k column: 02
High quality sequence stop: 728.

FEATURES
source

Location/Qualifiers
1. 904
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6278137"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.2%; Score 240; DB 13; Length 904;
Best Local Similarity 83.0%; Pred. No. 9.6e-52;
Matches 289; Conservative 0; Mismatches 50; Indels 9; Gaps 1;

QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCCTCAGCTGCTCTCT 63
Db 86 GAGTGGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCCTCAGCTGCTCTCT 145

QY 64 GGTGGCTCCATCCGAGTGGTGTATTATTGGAGTTGGTCCGCGAGCCCTCCAGGGAAG 123
Db 146 GGTGGCTCCATCAGCAGTAGTGTACTAGTGGGCTGGATCCGCGAGCCCTCCAGGGAAG 205

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTTACAAACCCGTCCTC 183
Db 206 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGGAGCACCCTACTACACCCGTCCTC 265

QY 184 AAGAGTCGAATTACATGTCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 266 AAGAGTCGAGTCACCATATCCGTAGACACGCTCCAAAGAACCACTTCTCCCTGAGCTGAGC 325

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGTCAAGTCTCTCTCTCTCTCA 294
Db 326 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGAGCAGCAGCAGCTGCTGTA 385

QY 295 TATACCTTTGGAACACTGGGGCCAGGGAACCCCTGTCACCGTCTCTCTCA 342
Db 386 CATTACTTCCAGCACTGGGGCCAGGCAACCCCTGTCACCGTCTCTCTCA 433

RESULT 10
BU899307

LOCUS BU899307 959 bp mRNA linear EST 17-OCT-2002
DEFINITION AGENCOURT 8532130 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280128
5', mRNA sequence.
ACCESSION BU899307
VERSION BU899307.1 GI:24081220
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 959)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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FEATURES
source

High quality sequence stop: 605.
Location/Qualifiers
1. 959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6280128"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 70.1%; Score 239.8; DB 13; Length 959;
Best Local Similarity 83.2%; Pred. No. 1.1e-51;
Matches 287; Conservative 0; Mismatches 52; Indels 6; Gaps 1;

QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCCTCAGCTGCTCTCT 63
Db 86 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCCTCAGCTGCTCTCT 145

QY 64 GGTGGCTCCATCCGAGTGGTGTATTATTGGAGTTGGTCCGCGAGCCCTCCAGGGAAG 123
Db 146 GGTGGCTCCATCAGCAGTAGTGTATTCTTCTGGAGTGGATCCGCGAGCTCTCCAGGGAAG 205

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTTACAAACCCGTCCTC 183
Db 206 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGGAGCACCCTACTACACCCGTCCTC 265

QY 184 AAGAGTCGAATTACATGTCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 266 AGGCGTCGAGTTACCATATCCTAGACACGCTCCAAAGAACCACTTCTCCCTGAGCTGAGC 325

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGCGTCAAGTCTCTCTCTCTCTCA 297
Db 326 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGAGATGGCAGCTCATGGGGT 385

QY 298 ACTTTGGACAACTGGGGCCAGGGAACCCCTGTCACCGTCTCTCTCA 342
Db 386 GCTTTTGATATCTGGGGCCAGGGAACATGTCACCGTCTCTCTCA 430

RESULT 11
BX324929

LOCUS BX324929 890 bp mRNA linear EST 02-MAY-2003
DEFINITION BX324929 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSOD1086YJ13 5-PRIME, mRNA sequence.
ACCESSION BX324929
VERSION BX324929.1 GI:30339413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 890)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7198.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOA1086CE070P1&cluster=7198.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genescope sequence ID : CS0A1086CE07QPI.
Location/Qualifiers
1. .890
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1086J13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="First strand cDNA was primed with a NotI-oligo (dfr)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES source

ORIGIN

Query Match 69.8%; Score 238.8; DB 13; Length 890;
Best Local Similarity 82.5%; Pred. No. 2e-51;
Matches 292; Conservative 0; Mismatches 47; Indels 15; Gaps 1;
Qy 4 GAGTCTGCCCGCAGACTGGTGAAGCCTTCAAGACCTTCCACCTGTCACCTGACCTGTCTCT 63
Db |||||
133 GAGTCGGGCCCGCAGACTGGTGAAGCCTTCCGAGACCTCTGCTCCCTCACCTGCACTGTCTCT 192
Qy 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCACCTCCAGGGAAG 123
Db |||||
193 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCACCTCCAGGGAAG 252
Qy 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTCAACAACCCCTGCCCTC 183
Db |||||
253 GGGCTGAGTGGATGGGACTATCTATTATAGTGGAGACACTACTACTAACCCCTGCCCTC 312
Qy 184 AAGAGTCCGATACCATGTCTAGTAGACACGTCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db |||||
313 AAGAGTCCGATACCATGTCTAGTAGACACGTCTTAAGAACCACTTCTCCCTGAGCTGAGC 372
Qy 244 TCTGTGACTCGCGGACACGGCGCTTATTACTGTGGCGGTGAGTGGTAT----- 297
Db |||||
373 TCTGTGACCGCGCGGACACGGCGCTTATTACTGTGCGAGTGGTGGTGGATGAGC 432
Qy 298 -----ACTTTGGACAACTGGGGCCAGGGAACCTGTGTCACCGTCTCCTCA 342
Db |||||
433 TGCTACCTCGCTTGACTACTGGGGCCAGGGAACCTGTGTCACCGTCTCCTCA 486

RESULT 12
BQ706579
LOCUS
DEFINITION AGENCOURT_8487944 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300935
5', mRNA sequence.
ACCESSION BQ706579
VERSION BQ706579.1 GI:21845478
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2515 row: p column: 24
High quality sequence start: 4

High quality sequence stop: 584.
Location/Qualifiers
1. .903
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6300935"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 69.6%; Score 238.2; DB 13; Length 903;
Best Local Similarity 82.9%; Pred. No. 2.8e-51;
Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;
Qy 4 GAGTCTGCCCGCAGACTGGTGAAGCCTTCAAGACCTTCCACCTGACCTGCTCTCT 63
Db |||||
98 GAGTCGGGCCCGCAGACTGGTGAAGCCTTCCGAGACCTGCTCCCTCACCTGCACTGTCTCT 157
Qy 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCACCTCCAGGGAAG 123
Db |||||
158 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCCACCTCCAGGGAAG 217
Qy 124 GGCCTGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTCAACAACCCCTGCCCTC 183
Db |||||
218 GGGCTGAGTGGATGGGAAATATCGATTATAGTGGGAGCATCTACTACAACCCCTGCCCTC 277
Qy 184 AAGAGTCCGATACCATGTCTAGTAGACACGTCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db |||||
278 AAGAGTCCGATACCATGTCTAGTAGACACGTCTTAAGAACCACTTCTCCCTGAGACTGAGG 337
Qy 244 TCTGTGACTCGCGGACACGGCGCTCTATTACTGTGC-----GCGGTGAGTGGGTAT 297
Db |||||
338 TCTGTGACCGCGGACACGGCGCTCTATTACTGTGGAAAGGGGCATAGTTATGGGC 397
Qy 298 ACTTTGAGAACCTGGGGCCAGGGAACCCGTGTCACCGTCTCCTCA 342
Db |||||
398 TGGTTCGACCCCTGGGGCCAGGGAACCCGTGTCACCGTCTCCTCA 442

RESULT 13

BM920469
LOCUS
DEFINITION AGENCOURT_6709612 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750444
5', mRNA sequence.
ACCESSION BM920469
VERSION BM920469.1 GI:19370848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLM12781 row: 9 column: 21
High quality sequence stop: 626.

FEATURES

source

1. 1108
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:575044"
/lab_host="DH10B"
/clone_lib="NIH_MGC_122"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 69.6%; Score 238.2; DB 12; Length 1108;
Best Local Similarity 82.9%; Pred. No. 3.1e-51;
Matches 286; Conservative 0; Mismatches 53; Indels 6; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
|||||
Db 110 GAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCTCACCTGCACTGTCTCT 169
|||||

QY 64 GGTGGCTCATCCGACAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCCTCCAGGGAAG 123
|||||
Db 170 GGTGGCTCCGTGACAGTGGTGGTTACTACTGGAGCTGGATCCGCGAGCCCCCAGGGAAG 229
|||||

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACCAACCCGTCCTC 183
|||||
Db 230 GGACTGGAGTGGATGGGTGATATCTATTACAGTGGGAGCACCACCTACAAACCCCTCCCTC 289
|||||

QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
|||||
Db 290 AAGAGTCGAGTCACCATATCAGTAGACACGCTCCAGAACCACTTCTCCCTGAGCTGAGC 349
|||||

QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGGCGGTGATAGTGGG-----TAT 297
|||||
Db 350 TCTGTGACCGGTGCGGACACGCGCGTGTATTACTGTGAGCGGGGGGGGGGAGACTAC 409
|||||

QY 298 ACTTTGGACAACCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
|||||
Db 410 TACATGGAGCTGTGGGGCAAGGAGCACCGGTGTCCTCTCA 454
|||||

RESULT 14

BX396901

LOCUS

DEFINITION BX396901 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI026YE08 5-PRIME, mRNA sequence.

ACCESSION

BX396901

VERSION

BX396901.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For

more information about this cluster, see

http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI026BC04Qp1&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI026BC04Qp1.

FEATURES

source

1. 977
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI026YE08"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 69.4%; Score 237.2; DB 13; Length 977;
Best Local Similarity 82.2%; Pred. No. 5.3e-51;
Matches 291; Conservative 0; Mismatches 48; Indels 15; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
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Db 163 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 222
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QY 64 GGTGGCTCATCCGACAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCCTCCAGGGAAG 123
|||||
Db 223 GGTGGCTCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCGAGCCCCCAGGGAAG 282
|||||

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACCAACCCGTCCTC 183
|||||
Db 283 GGACTGGAGTGGATGGGTGATCTATTACAGTGGGAGCACCACCTACAAACCCCTCCCTC 342
|||||

QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
|||||
Db 343 AAGAGTCGAGTCACCATATCAGTAGACACGCTCCAGAACCACTTCTCCCTGAGCTGAGC 402
|||||

QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGGG-----CGGTCA 288
|||||

Db 403 TCTGTGACCGCGCGAGACGCGCGTGTATTACTGTGCGATCACCAGATAGTGGCTAC 462
|||||

QY 289 GATGGGTATACCTTTGGACAACCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
|||||

Db 463 GATGAGGGCTTCTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 516
|||||

RESULT 15

BX336959

LOCUS

DEFINITION

BX336959

ACCESSION

VERSION

BX336959.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI034BE01QPI&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL : Corporation 1600
http://fulllength.invitrogen.com/ Invitrogen 1600
Faraday Avenue denoscope sequence ID : CS0DI034BE01QPI.

FEATURES

Location/Qualifiers
1. .1201
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DI034YI02"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 69.4%; Score 237.2; DB 13; Length 1201;
Best Local Similarity 82.2%; Pred. No. 5.8e-51;
Matches 291; Conservative 0; Mismatches 48; Indels 15; Gaps 1;
Qy 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCAAGACCCCTGTCCTCACTGCTCTCT 63
Db 156 GAGTCGGGCCAGGACTGGTGAAGCCTTCAAGACCCCTGTCCTCACTGCTCTCT 215
Qy 64 GGTGGCTCCATCCGAGTGGTGTATTATTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 123
Db 216 GGTGGCTCCATCAGCAGTGGTGTATTATTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 275
Qy 124 GGCCTGGAGTGGATCGGCAACATCTATCAGATGGCAACACTACAAACCCCTCCCTC 183
Db 276 GGACTGGAGTGGATGGCGGTATCTATACAGTGGGAGCACCACACTACACCCCTCCCTC 335
Qy 184 AAGAGTCGAATTACATGTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 336 AAGAGTCGAGTCAACATATCAGTAGACACGCTCCAGAACCACTTCTCCCTGAAGCTGAGC 395
Qy 244 TCTGTGACTCGCGGACACGCGCTTATTACTGTGGG-----CGGTCA 288
Db 396 TCTGTGACCGCGGACACGCGCTTATTACTGTGGGATCACCACCATAGTGGCTAC 455
Qy 289 GATGGGTATACCTTTGGACAACTGGGGCCAGGGAACCCCTGGTCAAGCTCTCCTCA 342
Db 456 GATGAGGGCTTGTGTGACTACTGGGGCCAGGGAACCCCTGGTCAAGCTCTCCTCA 509

Search completed: August 13, 2004, 07:13:19
Job time : 2007.71 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 222.818 Seconds
(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725a-2

Perfect score: 342

Sequence: 1 ctgagctgtgcccaggact.....ccctggctacgcgtctctctca 342

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	340.4	99.5	342	6	ABK89638 DNA encod
2	324.4	94.9	342	6	ABK89639 DNA encod
3	297.2	86.9	342	6	ABK89637 DNA encod
4	271.8	79.5	352	9	ADC99786 Anti-huma
5	271.8	79.5	352	9	Add05390 Anti-MUC1
6	268.4	78.5	360	4	Aaf29076 Human HIV
7	262.2	76.7	352	9	ADC99778 Anti-huma
8	262.2	76.7	352	9	Add05382 Anti-MUC1
9	260.4	76.1	358	9	ADC99798 Anti-huma
10	260.4	76.1	358	9	Add05402 Anti-MUC1
11	257.8	75.4	369	4	Aaf29046 Human HIV
12	254.8	74.5	352	9	ADC99806 Anti-huma
13	254.8	74.5	352	9	Add05410 Anti-MUC1
14	251.2	73.5	366	4	Aaf29066 Human HIV
15	251.2	73.5	516	3	Aaa46876 DNA encod
16	250.2	73.2	741	3	Aaz28998 Anti-muri
17	249.2	72.9	357	2	ABQ38670 MAB GAH V
18	247.8	72.5	467	7	Ab259692 Anti-TRAI
19	244.8	71.6	504	3	Aaz42341 Human 5'
20	244.6	71.5	467	7	Ab259694 Anti-TRAI
21	244.2	71.4	381	6	Abk24408 Heavy cha
22	244.2	71.4	1644	2	Aaz24434 Human bla
23	244	71.3	378	3	Aac62336 DNA encod

ALIGNMENTS

RESULT 1

ABK89638
ID ABK89638 standard; DNA; 342 BP.

XX ABK89638;

DT 21-OCT-2002 (first entry)

DE DNA encoding human IgE Fab clone 60 heavy chain.

KW Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.

OS Homo sapiens.

EH Key Location/Qualifiers

FT CDS 1..342 /tag= a

FT FT /product= "Fab clone 60 heavy chain"

FT FT misc_feature 7..78

FT FT /tag= b /note= "FR1 region"

FT FT misc_feature 79..99

FT FT /tag= c /note= "CDR1 region"

FT FT misc_feature 100..123

FT FT /tag= d /note= "FR2 region"

FT FT misc_feature 134..141

FT FT /tag= e /note= "FR3 region"

FT FT misc_feature 142..189

FT FT /tag= f /note= "CDR2 region"

FT FT misc_feature 190..285

FT FT /tag= g /note= "FR3 region"

FT FT misc_feature 286..309

FT FT /tag= h /note= "CDR3 region"

FT FT misc_feature 310..342

FT FT /tag= i /note= "FR4 region"

PN WO200253595-A1.

XX

Abk84446 Human CDN
Aca64884 Human Ig
Abs90024 Human mon
Abs46332 Human liv
Aaq78969 Human imm
Aaf29506 Human Fab
Abk24410 Heavy Cha
Abc98188 Human col
Abk24406 Heavy cha
Aaz42292 Human 5'
Aac66522 Human imm
Aav86218 EST clone
Aaz49608 DNA-1 rel
Aaz49590 Human ant
Aal50841 Human ant
Aaf97947 Human sec
Aaf29051 Human HIV
Aaz39316 Nucleotid
Ada89197 Human ant
Abt31873 Anti-CD40
Aas03405 DNA encod
Aaq33035 MAB 1-3-1

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PD 11-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-SE002908.
XX
PR 29-DEC-2000; 2000SE-00004892.
XX
PA (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
PI Flicker S, Steinberger P, Kraft D, Valenta R;
XX
DR WPI; 2002-583604/62.
DR P-PSDB; ABG30446.
XX
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
PT variable region of group 2 allergen specific-human IgE Fabs, useful for
PT diagnosing or passive immunotherapy of type I allergy, for environmental
PT allergen detection.
XX
XX
XX Disclosure; Page 32; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
CC allergen-specific human IgE Fabs and methods for their use. The proteins
CC of the invention may have antiallergic activities and may be used as a
CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
CC 2 allergen-specific fabs of the invention may be useful for environmental
CC allergen detection and for standardisation of allergen extracts. The fabs
CC - or a vaccine against a type I allergy is useful for passive
CC immunotherapy of type I allergy, it is also useful for diagnosing a type
CC I allergy. The allergen-specific fabs of the invention are useful for
CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
CC also useful for blocking the binding of grass pollen allergic patients
CC IgE antibodies to Phi p 2. The present sequence represents the DNA
CC encoding the human IgG fab, clone 60 heavy chain protein of the invention
XX
XX Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;
XX
XX Query Match
XX Best Local Similarity 99.5%; Score 340.4; DB 6; Length 342;
XX Matches 341; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 CTCGAGTCTGGCCCGAGGACTGGTGAAGCCTTCACAGACCTTCCTCCCTCACTGCCTGTC 60
Db |||||
QY 1 CTCGAGTCTGGCCCGAGGACTGGTGAAGCCTTCACAGACCTTCCTCCCTCACTGCCTGTC 60
Db |||||
QY 61 TCTGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGG 120
Db |||||
QY 61 TCTGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGG 120
Db |||||
QY 121 AAGGCGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACAAACCCGTC 180
Db |||||
QY 121 AAGGCGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACAAACCCGTC 180
Db |||||
QY 181 CTCAGAGTCTGAATTACATGTCAGTAGACAGCTTAAGAACCACTTCCTCCCTGAGACTG 240
Db |||||
QY 181 CTCAGAGTCTGAATTACATGTCAGTAGACAGCTTAAGAACCACTTCCTCCCTGAGACTG 240
Db |||||
QY 241 ACCTCTGTGACTGCGCGGACACCGCGTCTATTACTGTGGCGTCAAGTGGGTACT 300
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QY 241 ACCTCTGTGACTGCGCGGACACCGCGTCTATTACTGTGGCGTCAAGTGGGTACT 300
Db |||||
QY 301 TTGACAACTGGGGCCAGGGAACCTTGCTGTCACCGTCTCTCTCA 342
Db |||||
QY 301 TTGACAACTGGGGCCAGGGAACCTTGCTGTCACCGTCTCTCTCA 342
Db |||||
RESULT 2
ID ABK89639
XX ABK89639 standard; DNA; 342 BP.
AC ABK89639;
XX
```

```
CC IGE antibodies to Phi p 2. The present sequence represents the DNA
CC encoding the human IGE fab, clone 100 heavy chain protein of the
CC invention
XX
XX
SQ Sequence 342 BP; 69 A; 103 C; 94 G; 76 T; 0 U; 0 Other;

  Query Match      94.9%; Score 324.4; DB 6; Length 342;
  Best Local Similarity 96.8%; Pred. No. 1.4e-82;
  Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY      1 CTGAGTCTGCGCCAGGACTGGTGAAGCCTTTCAGAGCCCTGTCCCTCACCTGACACTGTC 60
DB      1 CTGAGTCTGCGCCAGGACTGGTGAAGCCTTTCAGAGCCCTGTCCCTCACCTGACACTGTC 60

QY      61 TCTGGTGGCTCCATCCGCGAGTGGTGGTATTATTGGAGTTGGGTCCGCGACGCTCCAGGG 120
DB      61 TCTGGTGGCTCCATCCGCGAGTGGTGGTATTATTGGAGTTGGATCCGCGACGCTCCAGGG 120

QY      121 AAGGCGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACACACCCCGTCC 180
DB      121 AAGGCGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACTACTACACCCCGTCC 180

QY      181 CTCAAGAGTCCGAATTACCATGTCTAGTAGACACAGCTTAAGAACCACTTCTCCCTGAGACTG 240
DB      181 CTCAAGAGTCCGATTACCATGTCTAGTAGACACAGCTTAAGAACCACTTCTCCCTGAGGCTG 240

QY      241 ACTCTCTGTACTGCGCGGACACGCGGTCTATTACTGTGGCGGTGAGATGGGTATACT 300
DB      241 AGCTCTGTGACTGCGCGGACACGCGGTGTATTACTGTGCGAGGTGAGATGGGTATACT 300

QY      301 TTGGACAACCTGGGCGGAGGAAACCCCTGTCACCGTCTCCCTCA 342
DB      301 TTGGACAACCTGGGCGGAGGAAACCCCTGTCACCGTCTCCCTCA 342

RESULT 3
ABK89637
ID   ABK89637 standard; DNA; 342 BP.
AC   ABK89637;
DT   21-OCT-2002 (first entry)
XX   DNA encoding human IGE Fab clone 94 heavy chain.
XX   Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
XX   timothy grass pollen allergen; passive immunotherapy.
XX   Homo sapiens.

FH   Key
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FT   1..342
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FT   /product= "Fab clone 94 heavy chain"
FT   misc_feature
FT   7..78
FT   /*tag= b
FT   /note= "FR1 region"
FT   misc_feature
FT   79..99
FT   /*tag= c
FT   /note= "CDR1 region"
FT   misc_feature
FT   100..123
FT   /*tag= d
FT   /note= "FR2 region"
FT   misc_feature
FT   134..141
FT   /*tag= e
FT   /note= "FR3 region"
FT   misc_feature
FT   142..189
FT   /*tag= f
FT   /note= "CDR2 region"
FT   misc_feature
FT   190..285
FT   /*tag= g
FT   /note= "FR3 region"
FT   misc_feature
FT   286..309
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FT
FT
FT   misc_feature
FT   310..342
FT   /*tag= i
FT   /note= "FR4 region"
XX
XX   WO200253595-A1.
XX
XX   11-JUL-2002.
XX
XX   27-DEC-2001; 2001WO-SB002908.
XX
XX   29-DEC-2000; 2000SB-00004892.
XX   (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
XX   Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX   WPI; 2002-583604/62.
XX   P-PSDB; ABG30445.
XX
XX   Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX   variable region of group 2 allergen specific-human IGE Fabs, useful for
XX   diagnosing or passive immunotherapy of type I allergy, for environmental
XX   allergen detection.
XX
XX   Disclosure; Page 31-32; 45pp; English.
XX
XX   This invention relates to the DNA and protein sequences of group 2
XX   allergen-specific human IGE Fabs and methods for their use. The proteins
XX   of the invention may have anti-allergic activities and may be used as a
XX   vaccine or an inhibitor of binding of grass pollen allergen patient's IGE
XX   antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX   2 allergen-specific Fabs of the invention may be useful for environmental
XX   allergen detection and for standardisation of allergen extracts. The Fabs
XX   - or a vaccine against a type I allergy is useful for passive
XX   immunotherapy of type I allergy, it is also useful for diagnosing a type
XX   I allergy. The allergen-specific Fabs of the invention are useful for
XX   inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX   also useful for identification of group 2 allergen-containing pollen and
XX   may be used for blocking the binding of grass pollen allergic patients
XX   IGE antibodies to Phi p 2. The present sequence represents the DNA
XX   encoding the human IGE fab, clone 94 heavy chain protein of the invention
XX
XX   Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;

  Query Match      86.9%; Score 297.2; DB 6; Length 342;
  Best Local Similarity 91.8%; Pred. No. 7.8e-75;
  Matches 314; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY      1 CTGAGTCTGCGCCAGGACTGGTGAAGCCTTTCAGAGCCCTGTCCCTCACCTGACACTGTC 60
DB      1 CTGAGTCTGCGCCAGGACTGGTGAAGCCTTTCAGAGCCCTGTCCCTCACCTGACACTGTC 60

QY      61 TCTGGTGGCTCCATCCGCGAGTGGTGGTATTATTGGAGTTGGGTCCGCGACGCTCCAGGG 120
DB      61 TCTGGCGGCTCCATCCGCGAGTGGTGGTATTACTTGGAGTTGGATCCGCGAACACCCAGGG 120

QY      121 AAGGCGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACACACCCCGTCC 180
DB      121 AAGGCGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACTACTACACCCCGTCC 180

QY      181 CTCAAGAGTCCGAATTACCATGTCTAGTAGACACAGCTTAAGAACCACTTCTCCCTGAGACTG 240
DB      181 CTCAAGAGTCCGAATTGCGATGTCTGAGTAGACAGCTTCTGAGAACCAAGTTCTCCCTGAGGCTG 240

QY      241 ACTCTCTGTACTGCGCGGACACGCGGTCTATTACTGTGGCGGTGAGATGGGTATACT 300
DB      241 AACTCTGTGACTGCGCGGACACGCGGTGTATTACTGTGCGAGGTAGATGGGTATACT 300

QY      301 TTGGACAACCTGGGCGGAGGAAACCCCTGTCACCGTCTCCCTCA 342
DB      301 TTGGACAACCTGGGCGGAGGAAACCCCTGTCACCGTCTCCCTCA 342
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```
RESULT 4
ID ADC99786
XX ADC99786 standard; DNA; 352 BP.
AC ADC99786;
DT 01-JAN-2004 (first entry)
DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.
XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human; ds; gene.
XX
OS Homo sapiens.
XX
PN WO2003057838-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041581.
XX
PR 28-DEC-2001; 2001US-0346299P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J;
XX
XX WPI; 2003-587113/55.
DR P-PSDB; ADC99784.
XX
XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
PS Claim 8; SEQ ID NO 15; 78pp; English.
XX
XX The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
XX heavy chain variable domain DNA of the invention.
XX
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 79.5%; Score 271.8; DB 9; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.4e-67;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCAGCTGTCTCT 63
Db 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCAGCTGTCTCT 75

QY 64 GGTGGCTCCATCCGACGTGGTGGTTATTATTGGAGTTGGGTCCGCGACGCTCCAGGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGGTTATTATTGGAGTTGGGTCCGCGACGCTCCAGGGGAAG 135

QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACCTACAAACCGTCCCTC 183
Db 136 GGCTGGAGTGGATGGGTTTCATCTATTACAGTGGAGCACTACTACAACCGTCCCTC 195

QY 184 AAGAGTCCGAATTACCATGTCACTAGACACGCTTAAAGAACCACTTCTCCCTGAGCTGACC 243
Db 196 AAGAGTCCGAGTTACCATATCATGATAGACACGCTTAGACACCACTTCTCCCTGAGCTGACC 255
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QY 244 TCTGTGACTGCGCGGACACGGCGCTATTACTGTGCGCGTCAAGTGGTATCTTTG 303
Db 256 TCTGTGACTGCGCGGACACGGCGCTATTACTGTGCGAG---AGAGGAGATGGCTTT 312

QY 304 GACAACTGGGGCCAGGGAACCTGTGTCACTGCTCTCTCA 342
Db 313 GACTACTGGGGCCAGGGAACCTGTGTCACTGCTCTCTCA 351

RESULT 5
ADD05390
ID ADD05390 standard; DNA; 352 BP.
XX
AC ADD05390;
XX
DT 01-JAN-2004 (first entry)
DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID NO 15.
XX monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
XX WPI; 2003-577496/54.
DR P-PSDB; ADD05388.
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX
PS Disclosure; SEQ ID NO 15; 87pp; English.
XX
XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.
XX
SQ Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match 79.5%; Score 271.8; DB 9; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.4e-67;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCAGCTGTCTCT 63
Db 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCAGCTGTCTCT 75
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QY 64 GGTGGCTCCATCCGACGTGGTGTATATATTTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 123
 Db 76 GGTGGCTCCATCCGACGTGGTGTATATTTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 135
 QY 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACACAAACCCGTCCTC 183
 Db 136 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACACAAACCCGTCCTC 195
 QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
 Db 196 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGAGC 255
 QY 244 TCTGTGACTCGCGGACACGGCCGCTCTATTACTGTGGCGGTGAGATGGGTATCTTTG 303
 Db 256 TCTGTGACTCGCGGACACGGCCGCTGTATTACTGTGCGAG---AGAGGGAGATGGCTTT 312
 QY 304 GACAACTGGGGCCAGGGAACCTCGTCACCGCTCTCCTCA 342
 Db 313 GACTACTGGGGCCAGGGAACCTCGTCACCGCTCTCCTCA 351

RESULT 6

AAF29076
 ID AAF29076 standard; DNA; 360 BP.

AC AAF29076;

XX 03-APR-2001 (first entry)

XX Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
 KW envelope glycoprotein; gp120; diagnosis; ds.

XX Homo sapiens.

XX WO200100678-A1.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-US017327.

XX 30-JUN-1999; 99US-0141701P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Watkins BA, Reitz MS;

XX WPI; 2001-112438/12.

XX P-PSDB; AAB62775.

XX Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
 PT in biological sample and providing passive immunotherapy to HIV-1
 PT infected mammal.

XX Claim 4; Page 45; 81pp; English.

XX The present invention provides the protein and coding sequences for the
 CC variable regions of human monoclonal antibodies which are immunoreactive
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
 CC These can be used in diagnosis and therapy of HIV-1 infection

XX Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

XX Best Match 78.5%; Score 268.4; DB 4; Length 360;

XX Best Local Similarity 88.6%; Pred. No. 1.3e-66;

XX Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCGACGAGTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGACATGTCTCT 63

Db 19 GAGTCTGGCCGACGAGTGGTGAAGCCTTCACAGACCTGTCCCTCAGCTGACATGTCTCT 78

QY 64 GGTGGCTCCATCCGACGTGGTGTATATATTTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 123
 Db 79 GGTGGCTCCATCCGACGTGGTGTATATTTGGAGTTGGGTCCGCCAGCCTCCAGGGAAG 138
 QY 124 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACACAAACCCGTCCTC 183
 Db 139 GGCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACACAAACCCGTCCTC 198
 QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
 Db 199 AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGAGC 258
 QY 244 TCTGTGACTCGCGGACACGGCCGCTCTATTACTGTGCG---CGGTGAGATGGGTATCT 300
 Db 259 TCTGTGACTCGCGGACACGGCCGCTGTATTACTGTGCGAGGGGTAGTAGTGGACTGG 318
 QY 301 TTGGACAACCTGGGGCCAGGGAACCTCGTCACCGCTCTCCTCA 342
 Db 319 TTGACCCCTGGGGCCAGGGAACCTCGTCACCGCTCTCCTCA 360

RESULT 7

ADC99778

ID ADC99778 standard; DNA; 352 BP.

AC ADC99778;

XX 01-JAN-2004 (first entry)

XX Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 7.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
 KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 KW lung cancer; human; ds; gene.

XX Homo sapiens.

XX WO2003057838-A2.

XX 17-JUL-2003.

XX 26-DEC-2002; 2002WO-US041581.

XX 28-DEC-2001; 2001US-0346299P.

XX (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

XX P-PSDB; ADC99776.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
 PT or condition associated with expression of MUC18 in a patient, e.g.
 PT tumors, cancers, and other malignancies.

XX Claim 8; SEQ ID NO 7; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising
 CC a heavy or light chain amino acid or a heavy or light chain variable
 CC domain where the antibody binds to MUC18. The monoclonal antibody of the
 CC invention demonstrates cytostatic activity and may be useful for treating
 CC a disease or condition associated with the expression of MUC18 on the
 CC cell surface such as tumours, specifically melanoma, oesophageal,
 CC pancreatic or colorectal tumours, carcinomas, particularly cervical
 CC carcinomas and cervical intraepithelial neoplasia and cancers including
 CC colorectal, breast or lung cancer, as well as other malignancies. The
 CC current sequence is that of the anti-human MUC18 monoclonal antibody
 CC heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 76.7%; Score 262.2; DB 9; Length 352;
Best Local Similarity 87.9%; Pred. No. 7.5e-65;
Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTGTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
DB 16 GAGTGGGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75

QY 64 GGTGCTCATCCGACGAGTGGTGTATTATTGGAGTTGGTCCGCGAGCTCCAGGGAAG 123
DB 76 GGTGCTCATCCGACGAGTGGTGTATTATTGGAGTTGGTCCGCGAGCTCCAGGGAAG 135

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTTC 183
DB 136 GGCCTGGAGTGGATGGGTGATCTATTACAGTGGAGGACCTACTACACCCGTCCTTC 195

QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAGTTTACCATATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGAGC 255

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGTGAGTGGGTATATTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGGGGGAGATGGCTAC 312

QY 304 GACAACTGGGGCCAGGGAAACCTGTCTACCGTCTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGGAAACCTGTCTACCGTCTCTCTCA 351

RESULT 8
ADD05382
ID ADD05382 standard; DNA; 352 BP.
XX AC ADD05382;
XX DT 01-JAN-2004 (first entry)
XX DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 7.
XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO2003057006-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041582.
XX PR 28-DEC-2001; 2001US-0346460P.
XX XX (ABGE-) ABGENIX INC.
XX PI Gudas J, Bar-Eli M;
XX DR WPI: 2003-577496/54.
XX DR P-PSDB; ADD05380.
XX
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
XX treating tumors, inhibiting tumor growth, inhibiting cell invasion
XX PT associated with melanoma, or increasing survival of an animal having a
XX PT metastatic tumor.
XX PS Disclosure; SEQ ID NO 7; 87pp; English.
XX
XX The invention relates to a novel monoclonal antibody used for inhibiting
XX tumor growth in an animal. The tumour inhibition process comprises
XX selecting an animal in need of treatment for a tumour, providing a
XX monoclonal antibody comprising a heavy chain amino acid, where the
XX antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumors, inhibiting tumor growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.

XX
SQ Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 76.7%; Score 262.2; DB 9; Length 352;
Best Local Similarity 87.9%; Pred. No. 7.5e-65;
Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTGTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
DB 16 GAGTGGGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75

QY 64 GGTGCTCATCCGACGAGTGGTGTATTATTGGAGTTGGTCCGCGAGCTCCAGGGAAG 123
DB 76 GGTGCTCATCCGACGAGTGGTGTATTATTGGAGTTGGTCCGCGAGCTCCAGGGAAG 135

QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACCCGTCCTTC 183
DB 136 GGCCTGGAGTGGATGGGTGATCTATTACAGTGGAGGACCTACTACACCCGTCCTTC 195

QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAGTTTACCATATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGAGC 255

QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGTGAGTGGGTATATTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG---AGGGGGAGATGGCTAC 312

QY 304 GACAACTGGGGCCAGGGAAACCTGTCTACCGTCTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGGAAACCTGTCTACCGTCTCTCTCA 351

RESULT 9
ADC99798
ID ADC99798 standard; DNA; 358 BP.
XX AC ADC99798;
XX DT 01-JAN-2004 (first entry)
XX DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 27.
XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
XX KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX KW lung cancer; human; ds; gene.
XX OS Homo sapiens.
XX PN WO2003057838-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041581.
XX PR 28-DEC-2001; 2001US-0346299P.
XX XX (ABGE-) ABGENIX INC.
XX PA Gudas J;
XX DR WPI: 2003-587113/55.
XX DR P-PSDB; ADC99796.

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XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX PS
XX PS Claim 8; SEQ ID NO 27; 78pp; English.
XX CC
XX CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
XX PS
XX PS Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;
XX
XX Query Match 76.1%; Score 260.4; DB 9; Length 358;
XX Best Local Similarity 87.1%; Pred. No. 2.4e-64;
XX Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
XX
XX QY 4 GAGCTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCAGTGTCTCT 63
XX Db 16 GAGTCTGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCAGTGTCTCT 75
XX
XX QY 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTGGGTCCGCCAGCCTCCAGGGAAG 123
XX Db 76 GGTGGCTCCATCAACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 135
XX
XX QY 124 GGCTGGAGTGGATTCGCAACATCTATCAGTGGCAACACCTACAAACCCCGTCCCTC 183
XX Db 136 GGCTGGAGTGGATTCGCAACATCTATCAGTGGCAACACCTACAAACCCCGTCCCTC 195
XX
XX QY 184 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
XX Db 196 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 255
XX
XX QY 244 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGCG---GTCAGATGGGTACT 300
XX Db 256 TCTATGACTGCGCGGACACGGCCGTCTATTACTGTGCGGAGAGATCGGGAACAGCTGGT 315
XX
XX QY 301 TTGGACAACCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
XX Db 316 TTTGACTACTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 357
XX
XX RESULT 10
XX ADD05402
XX ID ADD05402 standard; DNA; 358 BP.
XX AC ADD05402;
XX XX
XX XX Homo sapiens.
XX PN WO2003057006-A2.
XX XX
XX PD 17-JUL-2003.
XX XX
XX XX 26-DEC-2002; 2002WO-US041582.
XX XX
XX XX 28-DEC-2001; 2001US-0346460P.
XX PR
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XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Bar-Eli M;
XX DR WPI; 2003-577496/54.
XX DR P-PSDB; ADD05400.
XX
XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
PT metastatic tumor.
XX PS
XX PS Disclosure; SEQ ID NO 27; 87pp; English.
XX
XX CC The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.
XX
XX PS Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;
XX
XX Query Match 76.1%; Score 260.4; DB 9; Length 358;
XX Best Local Similarity 87.1%; Pred. No. 2.4e-64;
XX Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
XX
XX QY 4 GAGCTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCAGTGTCTCT 63
XX Db 16 GAGTCTGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCAGTGTCTCT 75
XX
XX QY 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTGGGTCCGCCAGCCTCCAGGGAAG 123
XX Db 76 GGTGGCTCCATCAACAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 135
XX
XX QY 124 GGCTGGAGTGGATTCGCAACATCTATCAGTGGCAACACCTACAAACCCCGTCCCTC 183
XX Db 136 GGCTGGAGTGGATTCGCAACATCTATCAGTGGCAACACCTACAAACCCCGTCCCTC 195
XX
XX QY 184 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
XX Db 196 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 255
XX
XX QY 244 TCTGTGACTGCGCGGACACGGCCGTCTATTACTGTGCGCG---GTCAGATGGGTACT 300
XX Db 256 TCTATGACTGCGCGGACACGGCCGTCTATTACTGTGCGGAGAGATCGGGAACAGCTGGT 315
XX
XX QY 301 TTGGACAACCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
XX Db 316 TTTGACTACTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 357
XX
XX RESULT 11
XX AAF29046
XX ID AAF29046 standard; DNA; 369 BP.
XX AC AAF29046;
XX XX
XX XX Homo sapiens.
XX PN WO2003057006-A2.
XX XX
XX PD 03-APR-2001 (first entry)
XX XX
XX XX Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 2.
XX XX
XX XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
```

KW envelope glycoprotein; gp120; diagnosis; ds.
 XX Homo sapiens.
 OS WO200100678-A1.
 PN 04-JAN-2001.
 PD 23-JUN-2000; 2000WO-US017327.
 PF 30-JUN-1999; 99US-0141701P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Watkins BA, Reitz MS;
 XX WPI; 2001-112438/12.
 DR P-PSDB; AAB62745.

XX Novel human monoclonal antibody immunoreactive with human

PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
 PT in biological sample and providing passive immunotherapy to HIV-1
 PT infected mammal.
 XX Claim 4; Page 34-35; 81pp; English.
 XX The present invention provides the protein and coding sequences for the
 CC variable regions of human monoclonal antibodies which are immunoreactive
 CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
 CC These can be used in diagnosis and therapy of HIV-1 infection
 XX Sequence 369 BP; 75 A; 104 C; 107 G; 83 T; 0 U; 0 Other;

Query Match 75.4%; Score 257.8; DB 4; Length 369;

Best Local Similarity 86.0%; Pred. No. 1.4e-63;

Matches 302; Conservative 0; Mismatches 37; Indels 12; Gaps 1;

QY 4 GAGTGTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGCTCTCT 63

DB 19 GAGTGTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGCTCTCT 78

QY 64 GTGTGCTCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 123

DB 79 GTGTGCTCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 138

QY 124 GSCCTGGAGTGGTACCGCAACATCTATCAGCTGGCAACCTACAAACCCGTCCTC 183

DB 139 GSCCTGGAGTGGTACCGCAACATCTATCAGCTGGCAACCTACAAACCCGTCCTC 198

QY 184 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243

DB 199 AAGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGACC 258

QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGGCGGTC-----AGAT 291

DB 259 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGGCGGCGCGTATTGTGGTGT 318

QY 292 GGGTATCTTTGGCAACTGGGGCCAGGGAACCCCTGGTCACCTGTCTCTCA 342

DB 319 GATTGCTCTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCTGTCTCTCA 369

RESULT 12

ID ADC99806

XX ADC99806 standard; DNA; 352 BP.

AC ADC99806;

XX 01-JAN-2004 (first entry)

XX Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 35.

XX anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;

KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
 KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
 KW lung cancer; human; ds; gene.

XX Homo sapiens.

OS WO2003057838-A2.

PN 17-JUL-2003.

PD 26-DEC-2002; 2002WO-US041581.

PF 28-DEC-2001; 2001US-0346299P.

PR (ABGE-) ABGENIX INC.

XX Gudas J;

XX WPI; 2003-587113/55.

DR P-PSDB; ADC99804.

XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease

PT or condition associated with expression of MUC18 in a patient, e.g.

PT tumors, cancers, and other malignancies.

XX Claim 8; SEQ ID NO 35; 78pp; English.

XX The invention relates to a novel isolated monoclonal antibody comprising

CC a heavy or light chain amino acid or a heavy or light chain variable

CC domain where the antibody binds to MUC18. The monoclonal antibody of the

CC invention demonstrates cytostatic activity and may be useful for treating

CC a disease or condition associated with the expression of MUC18 on the

CC cell surface such as tumours, specifically melanoma, oesophageal,

CC pancreatic or colorectal tumours, carcinomas, particularly cervical

CC carcinomas and cervical intraepithelial neoplasia and cancers including

CC colorectal, breast or lung cancer, as well as other malignancies. The

CC current sequence is that of the anti-human MUC18 monoclonal antibody

CC heavy chain variable domain DNA of the invention.

XX Sequence 352 BP; 77 A; 101 C; 105 G; 69 T; 0 U; 0 Other;

QY 5 AGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGCTCTCTG 64

DB 17 AGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCAGCTGCTCTCTG 76

QY 65 GTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAGG 124

DB 77 GTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAGG 136

QY 125 GCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACAAACCCGTCCTCTCA 184

DB 137 GCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACAAACCCGTCCTCTCA 196

QY 185 AGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGAGCT 244

DB 197 AGAGTCGAATTACCATGTCTAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTGAGCT 256

QY 245 CTGTGACTGCGCGGACACGCGCGTCTATTACTGTGGCGGTCAGATGGGTATAGTCTGGG 304

DB 257 CTGTGACTGCGCGGACACGCGCGTCTATTACTGTGGCGGTCAGATGGGTATAGTCTGGG 313

QY 305 ACAACTGGGGCCAGGGAACCCCTGGTCACCTGTCTCTCA 342

DB 314 GATACTGGGGCCAGGGAACCCCTGGTCACCTGTCTCTCA 351

RESULT 13

ID ADD05410

XX ADD05410 standard; DNA; 352 BP.


```
XX AC ADD05410;
XX DT 01-JAN-2004 (first entry)
XX DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID NO 35.
XX KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
XX KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO2003057006-A2.
XX PD 17-JUN-2003.
XX PF 26-DEC-2002; 2002WO-US041582.
XX PR 28-DEC-2001; 2001US-0346460P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J, Bar-Eli M;
XX DR WPI; 2003-577496/54.
XX DR P-PSDB; ADD05408.
XX PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
XX FT treating tumors, inhibiting tumor growth, inhibiting cell invasion
XX FT associated with melanoma, or increasing survival of an animal having a
XX FT metastatic tumor.
XX PS Disclosure; SEQ ID NO 35; 87pp; English.
XX CC The invention relates to a novel monoclonal antibody used for inhibiting
XX CC tumour growth in an animal. The tumour inhibition process comprises
XX CC selecting an animal in need of treatment for a tumour, providing a
XX CC monoclonal antibody comprising a heavy chain amino acid, where the
XX CC antibody consists of any one of 10 fully defined sequences of 117-123
XX CC amino acids given in the specification, and where the monoclonal antibody
XX CC binds MUC18, and contacting the tumour with the antibody resulting in
XX CC inhibited proliferation of the cells. The monoclonal antibody has
XX CC cytostatic and can be used in the production of a vaccine. The monoclonal
XX CC antibodies against the MUC18 antigen are useful for diagnosing and
XX CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
XX CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
XX CC increasing survival of an animal having a metastatic tumour. This
XX CC polynucleotide sequence represents the DNA encoding an anti-MUC18
XX CC antibody heavy chain, variable region, protein of the invention.
XX SQ Sequence 352 BP; 77 A; 101 C; 105 G; 69 T; 0 U; 0 Other;

Query Match 74.5%; Score 254.8; DB 9; Length 352;
Best Local Similarity 86.7%; Pred. No. 9.6e-63;
Matches 293; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

Qy 5 AGTCTGGCCAGGACTGTGTGAAGCTTTCACAGACCCCTGCTCCCTACCTGCACTGTCTCTG 64
Db 17 AGTCGGGCCAGGACTGTGTGAAGCTTTCAGAGACCCCTGCTCCCTACCTGCACTGTCTCTG 76

Qy 65 GTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGTCCGCGAGCTCCAGGGAAG 124
Db 77 GTGGCTCCATCAGCAGTGTGTTACTTACCACTGGAGTGGATCCGCGAGCACCAGGAGGG 136

Qy 125 GCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACCTACAAACCCGTCCTCTCA 184
Db 137 GCCTGGAGTGGATCGGCAACATCTATACAGTGGAGCACTACCAACCCGTCCTCTCA 196

Qy 185 AGAGTCGAATTACCATGTCAGTAGACACGCTTAGAACAACCTTCTCCCTGAGACTGACCT 244
Db 197 AGAGTCGAATTACCATATACGATAGACACGCTTAGAACAACCTTCTCCCTGAGACTGAGCT 256
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Qy 245 CTGTGACTGCGCGGCACACGCGCTCTATTACTGTGCGGTGATGGGTATCTTTGG 304
Db 257 CTGTGACGCGCGGCACACGCGCTGTATTACTGTGCGAG--AGGGGAGATGGCTACA 313

Qy 305 ACAACTGGGCGCAGGGAACCCCTGGTCAACCGCTCTCTCTCA 342
Db 314 GATACTGGGCGCAGGGAACCCCTGGTCAACCGCTCTCTCTCA 351

RESULT 14
AAF29066
ID AAF29066 standard; DNA; 366 BP.
XX AC AAF29066;
XX DT 03-APR-2001 (first entry)
XX DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 22.
XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX KW envelope glycoprotein; gp120; diagnosis; ds.
XX OS Homo sapiens.
XX PN WO200100678-A1.
XX PD 04-JAN-2001.
XX PF 23-JUN-2000; 2000WO-US017327.
XX PR 30-JUN-1999; 99US-0141701P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Watkins BA, Reitz MS;
XX DR WPI; 2001-112438/12.
XX DR P-PSDB; AAB62765.
XX PT Novel human monoclonal antibody immunoreactive with human
XX FT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX FT in biological sample and providing passive immunotherapy to HIV-1
XX FT infected mammal.
XX PS Claim 4; Page 42; 81pp; English.
XX CC The present invention provides the protein and coding sequences for the
XX CC variable regions of human monoclonal antibodies which are immunoreactive
XX CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX CC These can be used in diagnosis and therapy of HIV-1 infection
XX SQ Sequence 366 BP; 73 A; 107 C; 106 G; 80 T; 0 U; 0 Other;

Query Match 73.5%; Score 251.2; DB 4; Length 366;
Best Local Similarity 85.1%; Pred. No. 1e-61;
Matches 296; Conservative 0; Mismatches 43; Indels 9; Gaps 1;

Qy 4 GAGTCTGGCCAGGACTGTGTGAACCTTCAAGACCCCTGCTCCCTACCTGCACTGTCTCT 63
Db 19 GAGTCGGGCCAGGACTGTGTGAACCTTCAAGACCCCTGCTCCCTACCTGCACTGTCTCT 78

Qy 64 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGTCCGCGAGCTCCAGGGAAG 123
Db 79 GGTGGCTCCATCCGACGTGGTGGTATTATTGGAGTTGGATCCGCGAGCACCAGGGAAG 138

Qy 124 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGCAACACCTACAAACCCGTCCTC 183
Db 139 GGCCTGGAGTGGATCGGCAACATCTATACAGTGGGAGCACCCTACTACACCCGTCCTC 198

Qy 184 AAGAGTCGAATTACCATGTGTCAGTAGACACGCTTAGAACAACCTTCTCCCTGAGACTGACC 243
Db 199 AAGAGTCGAATTACCATATCAGTAGACACGCTTAGAACAACCTTCTCCCTGAGACTGAGC 258
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QY 244 TCTGTGACTGCGCGGACACCGCCGCTATTACTGTGCGCGG-----TCAGATGGG 294
Db 259 TCTGTGACTGCGCGGACACCGCGGTGTTATTACTGTGCGGAGGACATGCTACGGGACTCT 318
QY 295 TATACTTTGGACAACCTGGGGCGGAGGAACCCCTGGGTCAACCGTCTCTCTCA 342
Db 319 ACTGGACTGTGCTACTGCGGCGGTGGCACCCTGGTCACTGTCTCTCTCA 366

RESULT 15
AAA46876
ID AAA46876 standard; DNA; 516 BP.
XX
AC AAA46876;
XX
DT 03-OCT-2000 (first entry)
XX
DE DNA encoding the heavy chain of immunoglobulin clone 2.1.1.3.
XX
KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200037504-A2.
XX
PD 29-JUN-2000.
XX
PF 23-DEC-1999; 99WO-US030895.
XX
PR 23-DEC-1998; 98US-0113647P.
XX
PA (PFIZ ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
XX
DR WPI: 2000-442647/38.
DR P-PSDB; AAY93713.
XX
PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
PT treating, e.g. immune disorders.
XX
PS Example 2; Fig 1G; 157pp; English.
XX
CC The present sequence encodes a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a PRL-PR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDRI, CDRI and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders
XX
SQ Sequence 516 BP; 103 A; 167 C; 142 G; 104 T; 0 U; 0 Other;

Query Match 73.5%; Score 251.2; DB 3; Length 516;
Best Local Similarity 85.7%; Pred. No. 1.1e-61;
Matches 293; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

QY 7 TCTGGCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCTCCTGCACTGTCTCTGT 66
Db 1 TCGGGCCAGGACTGGTGAAGCTTCACAGATCCTGTCCTCCTGCACTGTCTCTGT 60
QY 67 GGCTCCATCCGAGTGGTGTATTATTGAGTTCGGTCCGCGAGCTCCAGGAGGGC 126
Db 61 GGCTCCATCAGCAGTGGTGTCTACTACTGAGCTGGATCCGCCAGCACCAGGAGGGC. 120
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QY 127 CTGGAGTGGATCGGCAACATCTTATCAAGTGGCAACACCTACAACACCCGTCCTCAAG 186
Db 121 CTGGAGTGGATGGGTATCATCTATTACATTGGGAACACTACTACAACCCGTCCTCAAG 180
QY 187 AGTCGAATTACCATGTCAAGTACAGACAGTCTAAGAACCACTTCTCCTGAGACTGACCTCT 246
Db 181 AGTCGAGTTACCATATATCAGTACAGACAGTCTAAGAACCACTTCTCCTGAGACTGAGCTCT 240
QY 247 GTGACTGCGGCGGACACCGCGCTCTATTACTGTGCGGTCAGATGGG-----TATACT 300
Db 241 GTGACTGCGGCGGACACCGCGGTGTATTATTGTGGAGAGATAGTGGGAGTACTACGGT 300
QY 301 TTGGACAACCTGGGGCGGAGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 301 ATAGACGTCTGGGGCGGAGGAGGACACCGTCAACCGTCTCTCTCA 342
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Search completed: August 13, 2004, 01:35:49
Job time : 223.818 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 03:58:10 ; Search time 760.173 Seconds
(without alignments)
2207.472 Million cell updates/sec

Title: US-10-027-725A-2

Perfect score: 342

Sequence: 1 ctgagctctggccaggact.....ccctgtaccgctctctca 342

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	342	100.0	342	15	US-10-027-725A-2
2	324.4	94.9	342	15	US-10-027-725A-3
3	298.8	87.4	342	15	US-10-027-725A-1
4	271.8	79.5	352	15	US-10-330-613-15
5	271.8	79.5	352	15	US-10-330-613-15
6	271.8	79.5	352	17	US-10-660-357-15
7	262.2	76.7	352	15	US-10-330-613-7
8	262.2	76.7	352	15	US-10-330-613-7
9	262.2	76.7	352	17	US-10-660-357-7
10	261.4	76.4	663	10	US-09-972-656-79
11	260.4	76.1	358	15	US-10-330-613-27
12	260.4	76.1	358	15	US-10-330-613-27
13	260.4	76.1	358	17	US-10-660-357-27
14	256.4	75.0	370	16	US-10-309-762-186
					Sequence 186, Appl
					Sequence 2, Appli
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 15, Appl
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 79, Appl
					Sequence 27, Appl
					Sequence 27, Appl
					Sequence 27, Appl
					Sequence 186, Appl

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15 255 74.6 429 16 US-10-309-762-110 Sequence 110, App
16 254.8 74.5 352 15 US-10-330-613-35 Sequence 35, Appl
17 254.8 74.5 352 15 US-10-330-613-35 Sequence 35, Appl
18 254.8 74.5 352 17 US-10-660-357-35 Sequence 35, Appl
19 252.6 73.9 361 16 US-10-309-762-191 Sequence 191, App
20 251.6 73.6 370 16 US-10-309-762-189 Sequence 189, App
21 250.6 73.3 370 16 US-10-309-762-185 Sequence 185, App
22 250.4 73.2 376 16 US-10-309-762-187 Sequence 187, App
23 249.4 72.9 352 16 US-10-309-762-203 Sequence 203, App
24 248.8 72.7 376 16 US-10-309-762-184 Sequence 184, App
25 248.8 72.7 376 16 US-10-309-762-197 Sequence 197, App
26 248.8 72.7 376 16 US-10-309-762-199 Sequence 199, App
27 248.4 72.6 519 16 US-10-309-762-174 Sequence 174, App
28 248.2 72.6 367 16 US-10-309-762-195 Sequence 195, App
29 245.2 71.7 370 16 US-10-309-762-200 Sequence 200, App
30 244.6 71.5 361 16 US-10-309-762-193 Sequence 193, App
31 244.2 71.4 381 17 US-10-312-316-66 Sequence 66, Appl
32 244.2 71.4 382 16 US-10-309-762-194 Sequence 194, App
33 244 71.3 378 9 US-09-974-449-5 Sequence 5, Appli
34 243 71.1 450 15 US-10-390-986-13 Sequence 13, Appl
35 242.6 70.9 324 9 US-09-864-761-31244 Sequence 31244, A
36 240.4 70.3 370 16 US-10-309-762-201 Sequence 201, App
37 240.4 70.3 370 16 US-10-309-762-212 Sequence 212, App
38 239.4 70.0 384 17 US-10-312-316-68 Sequence 68, Appl
39 239.2 69.9 393 9 US-09-925-299-198 Sequence 198, App
40 239.2 69.9 393 10 US-09-925-299-198 Sequence 198, App
41 237.8 69.5 381 17 US-10-312-316-64 Sequence 64, Appl
42 234.6 68.6 1543 9 US-09-800-729-74 Sequence 74, Appl
43 231.2 67.6 417 9 US-09-905-243-7 Sequence 41, Appl
44 231 67.5 360 13 US-10-371-942-41 Sequence 2, Appli
45 230.6 67.4 349 12 US-10-269-711-2 Sequence 2, Appli
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ALIGNMENTS

RESULT 1

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US-10-027-725A-2
; Sequence 2, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-2
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Query Match 100.0%; Score 342; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 4.6e-104;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CTGAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCTGCTCCCTCACTGCACGTGTC 60
Db 1 CTGAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCTGCTCCCTCACTGCACGTGTC 60
Qy 61 TCTGGTGGCTCCATCCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCCACCTCCAGGG 120
Db 61 TCTGGTGGCTCCATCCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCCACCTCCAGGG 120
Qy 121 AAGGCGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACCAACACCCGTC 180
Db 121 AAGGCGCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTACCAACACCCGTC 180
Qy 181 CTCAGAGTCGATTACCATCTCAGTAGACACGCTCTAAGAACCACTTCTCCCTGAGACTG 240
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Db 181 CTCAGAGTCGAATTAACATGTCAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTG 240
QY 241 ACCTGTGACTGCCCGGACAGCGGCTCTATTACTGTGGCGGTACAGATGGGTATCT 300
Db 241 ACCTGTGACTGCCCGGACAGCGGCTCTATTACTGTGGCGGTACAGATGGGTATCT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 342

RESULT 2

US-10-027-725A-3
; Sequence 3, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR APPLICATION NUMBER: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-3

Query Match 94.9%; Score 324.4; DB 15; Length 342;
Best Local Similarity 96.8%; Pred. No. 3.6e-98;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCCGGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTC 60
Db 1 CTCGAGTCTGGCCCGGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTC 60
QY 61 TCTGTGCTCCATCCGAGTGGTGTATTATTGAGTGGTGGCGGAGCTCCAGG 120
Db 61 TCTGTGCTCCATCCGAGTGGTGTATTATTGAGTGGTGGCGGAGCTCCAGG 120
QY 121 AAGGCCCTGGAGTGGTGAACATCTATACAGTGGCAACACCTACAAACCCGTC 180
Db 121 AAGGCCCTGGAGTGGTGAACATCTATACAGTGGCAACACCTACAAACCCGTC 180
QY 181 CTCAGAGTCGAATTAACATGTCAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTG 240
Db 181 CTCAGAGTCGAATTAACATGTCAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTG 240
QY 241 ACCTGTGACTGCCCGGACAGCGGCTCTATTACTGTGGCGGTACAGATGGGTATCT 300
Db 241 ACCTGTGACTGCCCGGACAGCGGCTCTATTACTGTGGCGGTACAGATGGGTATCT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 342

RESULT 3

US-10-027-725A-1
; Sequence 1, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR APPLICATION NUMBER: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-1

Query Match 87.4%; Score 298.8; DB 15; Length 342;
Best Local Similarity 92.1%; Pred. No. 1.3e-89;
Matches 315; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCCGGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTC 60
Db 1 CTCGAGTCTGGCCCGGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTC 60
QY 61 TCTGTGCTCCATCCGAGTGGTGTATTATTGAGTGGTGGCGGAGCTCCAGG 120
Db 61 TCTGTGCTCCATCCGAGTGGTGTATTACTGAGTGGATCCGCCAACACCCAGG 120
QY 121 AAGGCCCTGGAGTGGTGAACATCTATACAGTGGCAACACCTACAAACCCGTC 180
Db 121 AAGGCCCTGGAGTGGTGAACATCTATACAGTGGCAACACCTACAAACCCGTC 180
QY 181 CTCAGAGTCGAATTAACATGTCAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTG 240
Db 181 CTCAGAGTCGAATTAACATGTCAGTAGACAGCTTCTCCCTGAGACTG 240
QY 241 ACCTGTGACTGCCCGGACAGCGGCTCTATTACTGTGGCGGTACAGATGGGTATCT 300
Db 241 AACCTGTGACTGCCCGGACAGCGGCTGTATTACTGTGGAGGTAGATGGCTACT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 342

RESULT 4

US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match 79.5%; Score 271.8; DB 15; Length 352;
Best Local Similarity 89.7%; Pred. No. 1.5e-80;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTCCT 63
Db 16 GAGTGGGGCCCGGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACTGTCCT 75
QY 64 GGTGGTCCATCCGAGTGGTGTATTATTGAGTGGTGGCGGAGCTCCAGGGAAG 123
Db 76 GGTGGTCCATCAGCAGTGGTGGTATTACTGAGCTTGGATCCCGCAGCACCCAGGAAG 135
QY 124 GGCCTGGAGTGGTGGCAACATCTATCAGAGTGGCAACACCTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGTGGTTCATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 195

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184  AAGAGTCGAATTACATGTCTAGTAGACACGGTCTAAGAACCACTTCTCCCTGAGACTGACC 243
196  AAGAGTCGAGTTACCATATCATAGTAGACACGGTCTAAGAACCACTTCTCCCTGAGACTGACC 255
244  TCTGTGACTGCCGGCGGACACGGCCGCTCTATTACTGTGGCGGCTCAGATGGGTATACTTTG 303
256  TCTGTGACTGCCGGCGGACACGGCCGCTGTATTACTGTGGAG--AGAGGGAGATGGCTTT 312
304  GACAACTGGGGCCAGGGAAACCTGGTCAACCGTCTCCTCA 342
313  GACTACTGGGGCCAGGAAACCTGGTCAACCGTCTCCTCA 351

RESULT 5
US-10-330-530-15
; Sequence 15, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: AGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-15

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; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,590
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-15

Query Match          79.5%; Score 271.8; DB 17; Length 352;
Best Local Similarity 89.7%; Pred.No.1.5e-80;
Matches 304; Conservative 0; Mismatches 32; Indels 3; Gaps 1

QY    4   GAGTCTGGCCCCCAGACACTGGTGAAAGCCCTTCACAGAACCCCTGTGCCCTCACCGTGCACCTGCTCTCT 63
DB    16  GAGTCGGGCCCAAGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 75

QY    64  GTTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGGCAGCCTCCAGGGAAG 123
DB    76  GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGGACTTGGATCCGCCAAGCACCCAGGGAAG 135

QY    124 GCCCTGGAGTGATCGGCACAATCTATCACAGTGGCAACACTACAAACCCCGTCCCTC 183
DB    136 GGCTGTGGAGTGGATTTGGGTTTCATCTATTACAGTGGGAGCACTACTACACCCGTCCCTC 195

QY    184 AAGAGTCGAATTACCATGTCTAGTAGACACAGTCTTAAGAACCACCTTCTCCCTGAGACTGACC 243
DB    196 AAGAGTCGAGTTACCATATCAGTAGACACAGTCTTAAGAACCAGTTCTCCCTGAAGCTGAGC 255

QY    244 TCTGTGACTGCCGCGGACACGGCCGTCTATTACTGTGCGCGGTGAGATGGGTATACTTTTG 303
DB    256 TCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAG---AGAGGAGGATGGCTTT 312

QY    304 GACAACTGGGCCGAGGNAACCCCTGGTCACCGTCTCCCTCA 342
DB    313 GACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCCTCA 351

RESULT 7
US-10-330-613-7
; Sequence 7, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-7

Query Match          76.7%; Score 262.2; DB 15; Length 352;
Best Local Similarity 87.9%; Pred.No.2.4e-77;
Matches 298; Conservative 0; Mismatches 39; Indels 3; Gaps 1

QY    4   GAGTCTGGCCCAGGACTGGTGAAGCCCTTCACAGACCCTGTGCCCTCACCTGCACCTGCTCTCT 63
DB    16  GAGTCGGGCCCCAGGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 75

QY    64  GTTGGCTCCATCCGAGTGGTGGTTATTATTATTGGAGTTGGGTCCGGCAGCCTCCAGGGAAG 123
DB    76  GGTGGCTCCATCAGCAGTGGTGGTTACTTACACTGGAGCTGGATCCGCCAAGCACCCAGGGAAG 135

QY    124 GGCTGTGGAGTGATCGGCACAATCTATCACAGTGGCAACACTACAAACCCCGTCCCTC 183
```

Db 136 GGCCTGGAGTGAATGGGTACATCTATTACAGTGGAGACCTACTACAAACCGTCCCTC 195
QY 184 AAGAGTCGAATACCATGTCACTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTTACCATATACAGACAGCTCTAAGAACCTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGCTCAGATGGGTATACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG--AGGGGGAGATGGCTAC 312
QY 304 GACAACTGGGCGGACGAGAACCTTGGTCAACCGTCTCTCTCA 342
Db 313 AAGTACTGGGCGGACGAGAACCTTGGTCAACCGTCTCTCTCA 351

RESULT 8

US-10-330-530-7

; Sequence 7, Application US/10330530

; Publication No. US20030152514A1

; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean

; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES

; FILE REFERENCE: ABGENIX.031A

; CURRENT APPLICATION NUMBER: US/10/330,530

; PRIOR FILING DATE: 2002-12-26

; PRIOR APPLICATION NUMBER: US 60/346414

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 352

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-10-330-530-7

Query Match 76.7%; Score 262.2; DB 15; Length 352;

Best Local Similarity 87.9%; Pred. No. 2.4e-77;

Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCTGTCCCTCAGCTGACTGTCTCT 63
Db 16 GAGTGGGCGCCAGGACTGGTGAAGCCTTTCACAGACCTGTCCCTCAGCTGACTGTCTCT 75
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCGAGCCTCCAGGGAG 123
Db 76 GGTGCTCCATCAGCAGTGGTACTTACCACTGGAGTGGATCCGCGACACCCAGGGAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCAGCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATACCATGTCACTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTTACCATATCAGTAGACAGCTCTAAGAACCTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGCTCAGATGGGTATACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG--AGGGGGAGATGGCTAC 312
QY 304 GACAACTGGGCGGACGAGAACCTTGGTCAACCGTCTCTCTCA 342
Db 313 AAGTACTGGGCGGACGAGAACCTTGGTCAACCGTCTCTCTCA 351

RESULT 9

US-10-660-357-7

; Sequence 7, Application US/10660357

; Publication No. US20040115205A1

; GENERAL INFORMATION:

; APPLICANT: Bar-Eli, Menashe

; APPLICANT: Green, Lary L.

; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18

; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-7

Query Match 76.7%; Score 262.2; DB 17; Length 352;

Best Local Similarity 87.9%; Pred. No. 2.4e-77;

Matches 298; Conservative 0; Mismatches 38; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCTGTCCCTCAGCTGACTGTCTCT 63
Db 16 GAGTGGGCGCCAGGACTGGTGAAGCCTTTCACAGACCTGTCCCTCAGCTGACTGTCTCT 75
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCGAGCCTCCAGGGAG 123
Db 76 GGTGCTCCATCAGCAGTGGTACTTACCACTGGAGTGGATCCGCGACACCCAGGGAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACTACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCAGCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATACCATGTCACTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTTACCATATCAGTAGACAGCTCTAAGAACCTTCTCCCTGAGCTGACC 255
QY 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGCGGCTCAGATGGGTATACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGCGAG--AGGGGGAGATGGCTAC 312
QY 304 GACAACTGGGCGGACGAGAACCTTGGTCAACCGTCTCTCTCA 342
Db 313 AAGTACTGGGCGGACGAGAACCTTGGTCAACCGTCTCTCTCA 351

RESULT 10

US-09-972-656-79

; Sequence 79, Application US/09972656

; Publication No. US20030099647A1

; GENERAL INFORMATION:

; APPLICANT: Deshpande, Rajendra

; APPLICANT: Tsai, Mei-Mei

; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

; TITLE OF INVENTION: Neutralizing Activity

; FILE REFERENCE: A-799

; CURRENT APPLICATION NUMBER: US/09/972,656

; CURRENT FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 135

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 79

; LENGTH: 663

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(663)

US-09-972-656-79

Query Match

Best Local Similarity 76.4%; Score 261.4; DB 10; Length 663;

Matches 289; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCTGTCCCTCAGCTGACTGTCTCT 63
Db 16 GAGTGGGCGCCAGGACTGGTGAAGCCTTTCGAGAGACCTGTCCCTCAGCTGCGCTCTCT 75

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QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGGTGTATTCTCTGGAGCTGGATCCGGCAGCCACCGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTCAACAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATGGGTACATCTATCATGTGGAGCCTACTACAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTCACCATATCAGTAGACAGGTCCAAAGAACAGTTCTCCCTGAAGCTGAGC 255
QY 244 TCTGTGACTCCGCGGACACGGCCGCTATTACTGTGGCGGTGAGATGGGTATCTTTG 303
Db 256 TCTGTGACCGCGCGGACACGGCCGCTATTACTGTGCCAGAGGGGACTGGGGTACTTTT 315
QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTC 338
Db 316 GACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTC 350

RESULT 11
US-10-613-27
; Sequence 27, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-27

Query Match 76.1%; Score 260.4; DB 15; Length 358;
Best Local Similarity 87.1%; Pred. No. 9.5e-77;
Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
Db 16 GAGTCTGGCCCGCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGTCTTACTGGAGCTGGATCCGCCAGCCTCCAGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTCAACAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATGGGTACATCTATTCAGTGGAGCCTACTACAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATTACCTTATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAAGCTGAAC 255
QY 244 TCTGTGACTCCGCGGACACGGCCGCTATTACTGTGGCGG---GTGAGATGGGTACTACT 300
Db 256 TCTATGACTCCGCGGACACGGCCGCTATTACTGTGGAGAGATCGGGAACACAGCTGGT 315
QY 301 TTGGACACTGGGCCAGGGAACCCCTGGTCACCGTCTCTCA 342
Db 316 TTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCA 357

RESULT 12
US-10-330-530-27
; Sequence 27, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-27

Query Match 76.1%; Score 260.4; DB 17; Length 358;
Best Local Similarity 87.1%; Pred. No. 9.5e-77;
Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
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; Sequence 27, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-27

Query Match 76.1%; Score 260.4; DB 15; Length 358;
Best Local Similarity 87.1%; Pred. No. 9.5e-77;
Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCCGCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
Db 16 GAGTCTGGCCCGCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGTCTTACTGGAGCTGGATCCGCCAGCCTCCAGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACACCTCAACAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATGGGTACATCTATTCAGTGGAGCCTACTACAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATTACCTTATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAAGCTGAAC 255
QY 244 TCTGTGACTCCGCGGACACGGCCGCTATTACTGTGGCGG---GTGAGATGGGTACTACT 300
Db 256 TCTATGACTCCGCGGACACGGCCGCTATTACTGTGGAGAGATCGGGAACACAGCTGGT 315
QY 301 TTGGACACTGGGCCAGGGAACCCCTGGTCACCGTCTCTCA 342
Db 316 TTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCA 357

RESULT 13
US-10-357-27
; Sequence 27, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-27

Query Match 76.1%; Score 260.4; DB 17; Length 358;
Best Local Similarity 87.1%; Pred. No. 9.5e-77;
Matches 298; Conservative 0; Mismatches 41; Indels 3; Gaps 1;
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QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
Db 16 GAGTGGGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGGTTACTACTGGAGCTGGATCCGCGAGCACCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTACAGCAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTACAGCAACCCGTCCTC 195
QY 184 AAGAGTCGAATACCATTGCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATACCATTGCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGCCGCGGACACGGCCGTCTATTACTGTGCGCG---GTGAGATGGGTATCT 300
Db 256 TCTATGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATCGGGAACACAGTGGT 315
QY 301 TTGGACAACCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 316 TTGTACTAGTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 357

RESULT 14

US-10-309-762-186
; Sequence 186, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-186

Query Match 75.0%; Score 256.4; DB 16; Length 370;
Best Local Similarity 85.6%; Pred. No. 2.1e-75;
Matches 303; Conservative 0; Mismatches 36; Indels 15; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
Db 16 GAGTGGGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGAGTGGTGGTTACTACTGGAGCTGGATCCGCGAGCACCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTACAGCAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTACAGCAACCCGTCCTC 195
QY 184 AAGAGTCGAATACCATTGCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATACCATTGCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGCCGCGGACACGGCCGTCTATTACTGTGCGCGTCAAG----- 289
Db 256 TCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGCGGGGAATACTATGGT 315

QY 290 -ATGGGTATACCTTTGGACAACCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 316 TCGGGGAGTTACCTTGTACTACTTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 369

RESULT 15

US-10-309-762-110
; Sequence 110, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-110

Query Match 74.6%; Score 255; DB 16; Length 429;
Best Local Similarity 85.2%; Pred. No. 6.5e-75;
Matches 304; Conservative 0; Mismatches 35; Indels 18; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
Db 73 GAGTGGGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 132
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGAGCCTCCAGGGAAG 123
Db 133 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCGAGCACCAGGGAAG 192
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACCTTACAGCAACCCGTCCTC 183
Db 193 GGCCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCTC 252
QY 184 AAGAGTCGAATACCATTGCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 253 AAGAGTCGAATACCATTGCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGACTGACC 312
QY 244 TCTGTGACTGCCGCGGACACGGCCGTCTATTACTGTGCGCGTCAAGATGGGTATCTTTG 303
Db 313 TCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGAAATTACGATATTTG 372
QY 304 -----GACAACCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
Db 373 ACTGGTTTCAACTGGTTCGACCCCTGGGCGCAGGGAACCCCTGGTCAACCGTCTCTCTCA 429

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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	251.2	73.5	516	4	US-09-472-087-33
2	249.2	72.9	357	1	US-08-360-125-3
3	249.2	72.9	357	2	US-08-450-578-3
4	249.2	72.9	357	2	US-09-017-628-3
5	249.2	72.9	357	2	US-09-014-880-3
6	249.2	72.9	357	4	US-08-450-363-3
7	243	71.1	450	4	US-09-582-337-13
8	242.6	70.9	631	3	US-08-545-809A-31
9	237.4	69.4	1567	3	US-09-049-672A-17
10	234.6	68.6	1543	4	US-09-800-729-74
11	230.6	67.4	366	1	US-08-360-125-9
12	230.6	67.4	366	2	US-08-450-578-9
13	230.6	67.4	366	2	US-09-017-628-9
14	230.6	67.4	366	2	US-09-014-880-9
15	230.6	67.4	366	4	US-08-450-363-9
16	225	65.8	1212	3	US-08-545-809A-61
17	223.4	65.3	800	3	US-08-545-809A-39
18	215.6	63.0	750	4	US-10-039-785-62
19	215.2	62.9	403	3	US-09-042-353-357
20	215.2	62.9	403	4	US-08-758-417A-205
21	215	62.9	840	3	US-09-260-527-4
22	212	62.0	524	3	US-09-042-353-419
23	212	62.0	524	4	US-08-758-417A-219
24	212	62.0	4926	3	US-09-042-353-418
25	212	62.0	4926	4	US-08-758-417A-268
26	210.6	61.6	732	4	US-10-039-785-56
27	208	60.8	288	3	US-08-851-362D-7

Sequence 355, App
Sequence 203, App
Sequence 55, Appl
Sequence 45, Appl
Sequence 11, Appl
Sequence 20, Appl
Sequence 23, Appl
Sequence 28, Appl
Sequence 3, Appl
Sequence 7, Appl
Sequence 59, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 9, Appl
Sequence 5, Appl
Sequence 7, Appl
Sequence 9, Appl

28 207.8 60.8 404 3 US-09-042-353-355
29 207.8 60.8 404 4 US-08-758-417A-203
30 207.8 60.8 800 3 US-08-545-809A-55
31 207.6 60.7 381 2 US-08-477-553A-45
32 206.6 60.4 291 3 US-08-851-362D-11
33 205 59.9 357 2 US-08-652-816A-20
34 204.2 59.7 354 2 US-08-652-816A-23
35 204.2 59.7 624 3 US-08-545-809A-28
36 203.8 59.6 369 4 US-08-793-450-3
37 203.8 59.6 1418 4 US-08-793-450-7
38 203 59.4 622 3 US-08-545-809A-59
39 201.6 58.9 294 3 US-08-851-362D-3
40 201.4 58.9 650 3 US-08-545-809A-4
41 200.8 58.7 291 3 US-08-851-362D-9
42 200.2 58.5 402 1 US-08-259-372A-5
43 200.2 58.5 402 1 US-08-468-671-5
44 199.8 58.4 1404 3 US-08-523-894-7
45 199.8 58.4 1404 3 US-08-523-894-9

ALIGNMENTS

RESULT 1
US-09-472-087-33
; Sequence 33, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-087-33

Query Match 73.5%; Score 251.2; DB 4; Length 516;
Best Local Similarity 85.7%; Pred. No. 1.1e-68;
Matches 293; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

Qy 7 TCTGCCCCAGGACTGGTGAAGCCCTTCACAGACCCCTGTCCTCCTCAGCTGCTCTGGT 66
Db 1 TCGGGCCAGGACTGGTGAAGCCCTTCACAGATCTGTCCTCCTCAGCTGCTCTGGT 60

Qy 67 GGCTCCATCCGAGTGGTGGTATTATTGGAGTGGTCCGCCAGCTCCAGGGAAGGC 126
Db 61 GGCTCCATCAGCAGTGGTGGTCACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGC 120

Qy 127 CTGGAGTGGATCCGCACATCTATCATCAGTGGGGAACACCTACACACCCGTCCTCAAG 186
Db 121 CTGGAGTGGATGGGTGATCTATTATATTGGGGAACACCTACTACACCCGTCCTCAAG 180

Qy 187 AGTCGAATTACCATGTGAGTAGACACCTCTAAGAACCATCTTCTCCCTGAGACTGACCTCT 246
Db 181 AGTCGAGTTACCATATCAGTAGACACCTCTAAGAACCATCTTCTCCCTGAGACTGAGCTCT 240

Qy 247 GTGACTCCGCGGACACCGCGCTATTATGTGCGCGGTCCAGATGGG-----TACTACT 300
Db 241 GTGACTCCGCGGACACCGCGCTATTATTGTGCGGAGATAGTGGGGACTACTACGGT 300

QY 301 TTGACAACTGGGGCCAGGGAACCTGGTGCACCGTCTCTCA 342
Db 301 ATAGAGGCTGGGGCCAGGGAACCGTGCACCGTCTCTCA 342

RESULT 2

US-08-360-125-3
; Sequence 3, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLER:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:

CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-3

Query Match 72.9%; Score 249.2; DB 1; Length 357;
Best Local Similarity 85.1%; Pred. No. 4e-68;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCTCAGCTGCACTGCTCT 63
Db 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCTCAGCTGCACTGCTCT 75
QY 64 GGTGGCTCCATCCGCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGCAGCTCCAGGGGAAG 123
Db 76 GGTGGCTCCATCCGCGAGTGGTGGTTATTATTGGAGTTGGGTCCGCGCAGCTCCAGGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCAGTGGCAACACTACAAACCCGTCCTTC 183
Db 136 GGCCTGGAGTGGATTTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCTTC 195
QY 184 AAGAGTCGAATTACCATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAATTACCATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGCGCGTCAAGTGGGTATATTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTCTACCCGACTACGGGGG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACCAATGGTCAACCGTCTCTCA 357

RESULT 3

US-08-450-578-3
; Sequence 3, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb.

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,578

FILING DATE: May 25, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125

FILING DATE: December 20, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 357 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cdNA

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE: Hybridoma producing human

CELL TYPE: antibody GAH

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-578-3

Query Match

Best Local Similarity

Matches 291; Conservative

Score 249.2; DB 2; Length 357;

Pred. No. 4e-68;

Mismatches 0; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCTGTCCTCCTCACCTGCACTGTCTCT 63
DB 16 GAGTCGGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCTCCTCACCTGCACTGTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTTGAGTGGGTCCGCCAGCCTCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTGGTGGTTTCTTACTGGAAGTGGATCCGCCAGCACCAGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGGCAACACCTTACACACCCGTCCTC 183
DB 136 GGCTGGAGTGGATCGGCAACATCTATCAGTGGGCAACACCTTACACACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTGCTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAATTACCATGTGCTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGCCCGGACACGGCCGCTATTACTGTGGCGGTGAGATGGGTATCTTTG 303
DB 256 TCTGTGACTGCCCGGACACGGCCGCTATTACTGTGGCGGTGAGATGGGTATCTTTG 315
QY 304 ---GACAACTGGGGCCAGGGAACCTTGTACCGTCTCTCTCA 342
DB 316 GCTGACTACTGGGGCCAGGGAACATGGTACCGTCTCTCTCA 357

RESULT 4

US-09-017-628-3

Sequence 3, Application US/09017628

Patent No. 5990287

GENERAL INFORMATION:

APPLICANT: HOSOKAWA, Saiko

APPLICANT: TAGAWA, Toshiaki

APPLICANT: HIRAKAWA, Yoko

APPLICANT: ITO, No. 5990287hiko

APPLICANT: NAGAIKE, Kazuhiro

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO

FILE REFERENCE: 177/527361KH

CURRENT APPLICATION NUMBER: US/09/017,628

CURRENT FILING DATE: 1998-02-02

EARLIER APPLICATION NUMBER: 08/360,125

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 357

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Hybridoma producing human antibody GAH

US-09-017-628-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;

Best Local Similarity 85.1%; Pred. No. 4e-68;

Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCTGTCCTCCTCACCTGCACTGTCTCT 63
DB 16 GAGTCGGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCTCCTCACCTGCACTGTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTATTTGAGTGGGTCCGCCAGCCTCCAGGGAAG 123
DB 76 GGTGGCTCCATCAGCAGTGGTGGTTTCTTCTAGTGGATCCGCCAGCACCAGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGGCAACACCTTACAAACCCGTCCTC 183
DB 136 GGCTGGAGTGGATCGGCAACATCTATCAGTGGGCAACACCTTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTGCTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 243
DB 196 AAGAGTCGAATTACCATGTGCTAGACAGCTCTAAGAACCTTCTCCCTGAGACTGACC 255
QY 244 TCTGTGACTGCCCGGACACGGCCGCTATTACTGTGGCGGTGAGATGGGTATCTTTG 303

Db 256 TCTCTGAGTGGCGGACACGCGCGTGTATTACTGTGGAGGTCTACCGGACTACGGGGG 315
QY 304 ---GACAAGTGGCGGACGAGGACCTGTGTACCGGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACAATGGTCAACCGTCTCTTCA 357

RESULT 5

US-09-014-880-3
; Sequence 3, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 357 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

CELL TYPE: Hybridoma producing human

CELL TYPE: antibody G4H

US-09-014-880-3

Query Match 72.9%; Score 249.2; DB 2; Length 357;
Best Local Similarity 85.1%; Pred. No. 4e-68;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTCTCT 63

Db 16 GAGTGGGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACTGCACTGTCTCT 75

QY 64 GTGGCTCATCCGAGTGGTGGTTATTATTGGTTCGGTCCGCGCAGCCTCCAGGGAAG 123

Db 76 GTGGCTCATCAGCAGTGTGGTTTCTACTGGAACTGGATCCGCCAGCACCCAGGGAAG 135

QY 124 GSCCTGGAGTGGCAACATCTATCAGAGTGGCAACACCTACAACACCGTCCCTC 183
Db 136 GSCCTGGAGTGGATGGGTATCACTATTACAGTGGGAGCACCCTACTACACCCGTCCTC 195
QY 184 AAGAGTCGAATTTACCATGTCTAGTAGACACAGCTCTAAGAACCACCTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTTTACCATATCGCTAGACACAGCTCTAAGAGCCAGTCTTCTCCCTGAAGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTCTATTACTGTGGCGGTCTAGATGGGTATCTTTG 303
Db 256 TCTCTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGGTCTACCGGACTACGGGGG 315
QY 304 ---GACAACTGGGCGCAGGGAACCTGTGTACCGGTCTCTCTCA 342
Db 316 GCTGACTACTGGGCGCAGGGAACAATGGTCAACCGTCTCTTCA 357

RESULT 6

US-08-450-363-3
; Sequence 3, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Cell Membrane

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 357 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

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; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-08-450-363-3

Query Match
Best Local Similarity 72.9%; Score 249.2; DB 4; Length 357;
Matches 291; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 63
Db 16 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTATTATTTAGAGTTGGTCCGACAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTTGGTGGTCTTACTGGAATGGATCGGACGACCCAGGGAAG 135
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGGCAACACCTACAAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATGGGTACATCTATCAGTGGGCAACCTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCGAGTTACCATATCGCTAGACACAGCTTAAAGAGCAGTTCTCCCTGAAGCTGAGC 255
QY 244 TCTGTGACTCCGCGGACACGCGGCTCTATCTAGTCCGCGGTCCAGATGGGTACTTTG 303
Db 256 TCTGTGACTCCGCGGACACGCGGCTGTATTACTGTGCGAGGTCTACCCGACTACGGGG 315
QY 304 ---GACAACTGGGCGGAGGAAACCCCTGGTCACCGTCTCCTCA 342
Db 316 GCTGACTACTGGGCGGAGGAAACATGCTACCGTCTCCTCA 357

RESULT 7
US-09-582-337-13
; Sequence 13, Application US/09582337
; Patent No. 6562618
; GENERAL INFORMATION:
; APPLICANT: Japan Tobacco, Inc.
; TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
; TITLE OF INVENTION: and Medicinal Uses Thereof
```

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; FILE REFERENCE: J1-009PCT
; CURRENT APPLICATION NUMBER: US/09/582,337
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: JP P1997-367699
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP P1998-356183
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(450)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: V region
; LOCATION: (59)..(353)
; US-09-582-337-13

Query Match
Best Local Similarity 71.1%; Score 243; DB 4; Length 450;
Matches 303; Conservative 0; Mismatches 35; Indels 19; Gaps 2;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 63
Db 74 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGT-CCTCACCTGCACTGCTCT 132
QY 64 GGTGGCTCCATCCGAGTGGTGGTATTATTTAGAGTTGGTCCGACAGCCTCCAGGGAAG 123
Db 133 GGTGGCTCCATCAGCAGTTGGTGGTACTTACTGAGTGGATCCGACGACCCAGGGAAG 192
QY 124 GGCTGGAGTGGATCGGCAACATCTATCAGTGGGCAACACCTACAAACCCGTCCTC 183
Db 193 GGCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 252
QY 184 AAGAGTCGAATTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 253 AAGAGTCGAGTTACCATATCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAAGCTGAGC 312
QY 244 TCTGTGACTCCGCGGACACGCGGCTCTATTACTGTGCGGTCAGATGGGTACT-- 300
Db 313 TCTGTGACTCCGCGGACACGCGGCTGTATTACTGTGCGAGTATTACTATGATAGTGGT 372
QY 301 -----TTGGACAACTGGGCGGAGGAAACCCCTGGTCACCGTCTCCTCA 342
Db 373 GGTATTACGACTACTTTGACTACTGGGCGGAGGAAACCCCTGGTCACCGTCTCCTCA 429

RESULT 8
US-08-545-809A-31
; Sequence 31, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
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;; PRIOR APPLICATION NUMBER: 60/155,709
;; PRIOR FILING DATE: 1999-09-24
;; NUMBER OF SEQ ID NOS: 217
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 74
;; LENGTH: 1543
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-800-729-74

Query Match 68.6%; Score 234.6; DB 4; Length 1543;
Best Local Similarity 81.0%; Pred. No. 2.5e-63;
Matches 273; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 GAGTCTGGCCAGACAGTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCT 63
Db 90 GAGTCGGGCCAGACAGTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCT 149

Qy 64 GGTGGCTCCATCCGACAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 150 GGTGGCTCCATCAGAGTGGTGGTCACTACTGGAGCTGGATCCGCCAGACCCAGGGAAG 209

Qy 124 GGCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACACTACAAACCCGTCCTC 183
Db 210 GGCCTGGAGTGGATGGGTACATCTTTACAATGGGGTCACTACTACAATCCGTCCTC 269

Qy 184 AAGAGTCGAATTACATGTCTAGTACACAGCTCTAAGAACCACTTCTCCCTGAGACTGACC 243
Db 270 AAGAGTCGAGTTACCATATCTGTAGACACGCTCTCAGAACCACTTCTCCCTGAGCTGAGC 329

Qy 244 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGGCGGTGAGTGGGTATCTTTG 303
Db 330 TCTGTGACTGCGCGGACACGCGCTCTATTACTGTGGCGGAAGATCATCGAGGACACAGA 389

Qy 304 GACAACTGGGCCAGGGAACCTCGTCACCTCTCTCT 340
Db 390 GACGGTACCAGCTGGAATACCGAGGCTTTGACTACT 426

RESULT 11
US-08-360-125-9
; Sequence 9, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESS: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 366 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE: Hybridoma producing human antibody 1-3-1
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-9

Query Match 67.4%; Score 230.6; DB 1; Length 366;
Best Local Similarity 81.2%; Pred. No. 2.4e-62;
Matches 285; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

Qy 4 GAGTCTGGCCAGACAGTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCT 63
Db 16 GAGTCGGGCCAGACAGTGGTGAAGCCTTCGAGACCCCTGCTCCCTCAGCTGCTCTCT 75

Qy 64 GGTGGCTCCATCCGACAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTAGTACTACTGGGGCTGGATCCGCCAGACCCCGGAGGAAG 135

Qy 124 GGCTGGAGTGGATCGGCAACATCTATCAGAGTGGCAACACTTACACACACCCGTCCTC 183
Db 136 GGGCTGGAGTGGATGGGAGTATCTATTATAGTGGGAGCACCTACTACAAACCCGTCCTC 195

Qy 184 AAGAGTCGAATTACATGTCTAGTACACGCTCTAAGAACCCACTTCTCCCTGAGACTGACC 243

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QY 244 TCTGTGACTGCGCGGACAGCGCTCTATTACTGTGG-----CGGTGAGAT 291
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QY 292 GGGTATACTTTGGCAAACTGGGGCCAGGGAACCTGGTCACCGTCTCCTCA 342
Db 316 TACTACGGTATGGACGCTCTGGGGCCAAAGGACCACGGTCACGCTCTCCTCA 366

RESULT 12

US-08-450-578-9

; Sequence 9, Application US/08450578

; Patent No. 5837845

; GENERAL INFORMATION:

; APPLICANT: Saiko HOSOKAWA

; APPLICANT: Toshiaki TAGAWA

; APPLICANT: Yoko HIRAKAWA

; APPLICANT: No. 5837845ihiko ITO

; APPLICANT: Kazuhiro NAGAIKE

; TITLE OF INVENTION: Human Monoclonal Antibody

; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

; TITLE OF INVENTION: Cell Membrane

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wenderoth, Lind & Ponack

; STREET: 805 Fifteenth Street, N.W., #700

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,578

; FILING DATE: May 25, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/360,125

; FILING DATE: December 20, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/905,534

; FILING DATE: June 29, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warren M. Cheek, Jr.

; REGISTRATION NUMBER: 33,367

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-8850

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 366 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

; ORGANISM:

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

; TISSUE TYPE:

; CELL TYPE: Hybridoma producing human antibody 1-3-1

; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-9

Query Match 67.4%; Score 230.6; DB 2; Length 366;

Best Local Similarity 81.2%; Pred. No. 2.4e-62;

Matches 285; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

QY 4 GAGTCTGCGCCAGGACTGGTGAAGCCTTACAGAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
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Db 196 AAGAGTCGAGTCACCATATCGTAGACACAGTCCAGAACAGTTCCTCTGAGAGCTGAGC 255
QY 244 TCTGTACTGCGCGGACACCGCCGTCTATTACTGTGCG-----CGGTGAGAT 291
Db 256 TCTGTGACCGCGGACAGACACGGCTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC 315
QY 292 GGGTATACTTTGGCAAACTGGGGCCAGGGAACCCCTGGTCACGTCTCCTCA 342
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RESULT 13

US-09-017-628-9

; Sequence 9, Application US/09017628

; Patent No. 5990287

; GENERAL INFORMATION:

; APPLICANT: HOSOKAWA, Saiko

; APPLICANT: TAGAWA, Toshiaki

; APPLICANT: HIRAKAWA, Yoko

; APPLICANT: ITO, No. 5990287ihiko

; APPLICANT: NAGAIKE, Kazuhiro

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO

; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE

; FILE REFERENCE: 177/527361KH

; CURRENT APPLICATION NUMBER: US/09/017,628

; CURRENT FILING DATE: 1998-02-02

; EARLIER APPLICATION NUMBER: 08/360,125

EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 366
TYPE: DNA
ORGANISM: Unknown
FEATURES:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-9

Query Match 67.4%; Score 230.6; DB 2; Length 366;
Best Local Similarity 81.2%; Pred. No. 2.4e-62;
Matches 285; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

Qy 4 GAGTCTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCTGCCCCAGGACTGGTGAAGCCTTCGAGAGCCCTGCTCCCTCACCTGCACTGTCTCT 75

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Qy 184 AAGAGTCCGAATTACCATGTCTAGTAGACACGCTTAAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCCGATCACCATCGTAGACACGCTTAAAGAACCACTTCTCCCTGAGACTGACC 255

Qy 244 TCTGTGACTCGCGGACACGGCGCTTATTACTGTGGG-----CGGTGAGAT 291
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RESULT 14
US-09-014-880-9
Sequence 9, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-9

Query Match 67.4%; Score 230.6; DB 2; Length 366;
Best Local Similarity 81.2%; Pred. No. 2.4e-62;
Matches 285; Conservative 0; Mismatches 54; Indels 12; Gaps 1;

Qy 4 GAGTCTGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCTGCCCCAGGACTGGTGAAGCCTTCGAGAGCCCTGCTCCCTCACCTGCACTGTCTCT 75

Qy 64 GGTGGCTCCATCCGACGTGGTGTATATTATGGAGTTGGTCCGCGAGCCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATATTATGGAGTTGGTCCGCGAGCCTCCAGGGAAG 135

Qy 124 GGCTCTGAGTGGATCGGCAACATCTATCAGAGTGGCAACCTACCAACCCGTCCTC 183
Db 136 GGGCTGGAGTGGATCGGCAACATCTATTTAGTGGAGCCTACTACACCCGTCCTC 195

Qy 184 AAGAGTCCGAATTACCATGTCTAGTAGACACGCTTAAAGAACCACTTCTCCCTGAGACTGACC 243
Db 196 AAGAGTCCGATCACCATCGTAGACACGCTTAAAGAACCACTTCTCCCTGAGACTGACC 255

Qy 244 TCTGTGACTCGCGGACACGGCGCTTATTACTGTGGG-----CGGTGAGAT 291
Db 256 TCTGTGACTCGCGGACACGGCGCTTATTACTGTGGGAGGAGCTACGGGGGGCTAC 315

Qy 292 GGGTATATCTTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 342
Db 316 TACTACGATAGGACGCTGGGGCCAGGGAACCCGTCACCGTCTCTCTCA 366

RESULT 15
US-08-450-363-9
Sequence 9, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-363-9

Query Match 67.4%; Score 230.6; DB 4; Length 366;
Best Local Similarity 81.2%; Pred. No. 2.4e-62;
Matches 285; Conservative 54; Mismatches 54; Indels 12; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCCCTGTCCTCACCTGCACCTGTCTCT 63
DB 16 GAGTCGGGCCAGGACTGGTGAAGCTTCGGGAGACCCCTGTCCTCACCTGCACCTGTCTCT 75

QY 64 GGTGGCTCCATCCGCAAGTGGTGTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCGCAAGTGGTGTATTATTGGAGTTGGTCCGCCAGCTCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACACCTACAAACACCCGTCCTTC 183
DB 136 GGGCTGGAGTGGATTTGGGAGTATCTATTATAGTGGGAGCACCTACTACAACCCGTCCTTC 195
QY 184 AAGAGTCGAATTACCATGTCTAGTAGACAGGCTTAAGAACCACTTCTCCGTGAGACTGACC 243
DB 196 AAGAGTCGAGTCACCATATCCGTAGACACGTCCTCAAGAACCACTTCTCCGTGAGACTGACC 255
QY 244 TCTGTGACTGCGCGGACACGSCGTCTATTACTGTGCG-----CGGTCAAGAT 291
DB 256 TCTGTGACCGCGGACACGCGTGTGTATTACTGTGAGGGGAGCTACGGGGGCTAC 315
QY 292 GGGTATACCTTTGGCAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
DB 316 TACTACGGTATGGACGTCTGGGGCCCAAGGGACCAAGGTACCGGTACCGTCTCTCTCA 366

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-027-725A-3
Perfect score: 342
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	332.8	94.4	342	9	HSA458383	AJ458383 Homo sapi
3	308.4	90.2	342	9	HSA458382	AJ458382 Homo sapi
4	284.6	83.2	414	9	AF062112	AF062112 Homo sapi
5	284.4	83.2	351	9	HSA244930	AJ244930 Homo sapi
6	284.4	83.2	360	6	AX061463	AX061463 Sequence
7	283.6	82.9	411	9	HST22X1	Z75385 H.sapiens m
8	283	82.7	354	9	HSA245064	AJ245064 Homo sapi
9	283	82.7	360	9	HSU80129	U80129 Human immu
10	283	82.7	360	9	HSU80130	U80130 Human immu
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37	271.6	79.4	357	9	HSA279530	AJ279530 Homo sapi
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ALIGNMENTS

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LOCUS HSA458384 342 bp mRNA linear PRI 30-APR-2002
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV gene), clone 100.
ACCESSION AJ458384
VERSION AJ458384.1 GI:20387067
KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y., Valent,P., Kraft,D. and Valenta,R.

```

TITLE      Conversion of grass allergen-specific human IgE into a protective
JOURNAL    IgG1 antibody
AUTHORS    Unpublished
REFERENCE  2 (bases 1 to 342)
TITLE      Flicker,S.
JOURNAL    Direct Submission
AUTHORS    Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
REFERENCE  General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
JOURNAL    Vienna, AUSTRIA

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Best Local Similarity 99.4%; Pred. No. 2.7e-86;
Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 181 CTCAGAGTCGAGTTACCATGTCAGTGGCAACACCTTCTCCCTGAGGCTG 240
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QY 241 AGCTCTGTGACTGCCGCGACACCGCGGTATTACTGTGCGAGGTCAGATGGTACACT 300
DB 241 AGCTCTGTGACTGCCGCGACACCGCGGTATTACTGTGCGAGGTCAGATGGTACACT 300

QY 301 TTGGACAACTGGGGCCAGGAAACCCCTGGTCACCGTCTCCTCA 342
DB 301 TTGGACAACTGGGGCCAGGAAACCCCTGGTCACCGTCTCCTCA 342

RESULT 2
LOCUS     HSA458383
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable
           region (IGHV gene), clone 60.
ACCESSION AJ458383
VERSION    AJ458383.1 GI:20387065
KEYWORDS  IGHV gene; immunoglobulin heavy chain; variable region.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           1
           Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
           Valent,P., Kraft,D. and Valenta,R.
           Conversion of grass allergen-specific human IgE into a protective
           IgG1 antibody
           Unpublished
           2 (bases 1 to 342)
           Flicker,S.
           Direct Submission
           Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
           General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
           Vienna, AUSTRIA
           Location/Qualifiers
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           /organism="Homo sapiens"
           /mol_type="mRNA"
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Query Match      94.4%; Score 322.8; DB 9; Length 342;
Best Local Similarity 96.5%; Pred. No. 1.1e-81;
Matches 330; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CTCGAGTCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCCACCTGCACCTGTC 60
DB 1 CTCGAGTCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCCACCTGCACCTGTC 60

QY 61 TCTGTGGTCCATCCGACGAGTGGTATTACTGGAGTTGGATCGCCAGCGTCCAGGG 120
DB 61 TCTGTGGTCCATCCGACGAGTGGTATTACTGGAGTTGGATCGCCAGCGTCCAGGG 120

QY 121 AAGGCGCTGGAGTGGTACCATGTCAGTGGCAACACCTTCTCCCTGAGGCTG 180
DB 121 AAGGCGCTGGAGTGGTACCATGTCAGTGGCAACACCTTCTCCCTGAGGCTG 180

QY 181 CTCAGAGTCGAGTTACCATGTCAGTGGCAACACCTTCTCCCTGAGGCTG 240
DB 181 CTCAGAGTCGAGTTACCATGTCAGTGGCAACACCTTCTCCCTGAGGCTG 240

QY 241 AGCTCTGTGACTGCCGCGACACCGCGGTATTACTGTGCGAGGTCAGATGGTACACT 300
DB 241 AGCTCTGTGACTGCCGCGACACCGCGGTATTACTGTGCGAGGTCAGATGGTACACT 300

QY 301 TTGGACAACTGGGGCCAGGAAACCCCTGGTCACCGTCTCCTCA 342
DB 301 TTGGACAACTGGGGCCAGGAAACCCCTGGTCACCGTCTCCTCA 342

RESULT 3
LOCUS     HSA458382
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable
           region (IGHV gene), clone 94.
ACCESSION AJ458382
VERSION    AJ458382.1 GI:20387063
KEYWORDS  IGHV gene; immunoglobulin heavy chain variable
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           1
           Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
           Valent,P., Kraft,D. and Valenta,R.
           Conversion of grass allergen-specific human IgE into a protective
           IgG1 antibody
           Unpublished
           2 (bases 1 to 342)
           Flicker,S.
           Direct Submission
           Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
           General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
           Vienna, AUSTRIA
           Location/Qualifiers
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ORIGIN
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KEYWORDS IGHV gene; immunoglobulin heavy chain; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Flicker, S., Steinberger, P., Norderhaug, L., Sperr, W.R., Majlesi, Y.,
 Valent, P., Kraft, D. and Valenta, R.
 TITLE Conversion of grass allergen-specific human IgE into a protective
 IgG1 antibody
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 342)
 AUTHORS Flicker, S.
 TITLE Direct Submission
 JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
 General Hospital of Vienna, 30, Waehringer Guertel 18-20, A-1090
 Vienna, AUSTRIA
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 1. .342
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 /clone="94"
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 /product="immunoglobulin heavy chain"
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 /db_xref="GI:20387064"
 /db_xref="RENTREMBL:CAD30444"
 /translation="LESGPLVKAQTLISCAVGSIRSGGYNSWIRHPKGLG
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 /gene="IGHV"
 /product="immunoglobulin heavy chain variable region"
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 Query Match 90.2%; Score 308.4; DB 9; Length 342;
 Best Local Similarity 93.9%; Pred. No. 1.5e-77;
 Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
 QY 1 CTCGAGTCTGGCCAGACCTGGTGAAGCTTACAGACCCCTGTCCTCAGCTGGCTGTC 60
 DB |||||||
 1 CTCGAGTCTGGCCAGACCTGGTGAAGCTTACAGACCCCTGTCCTCAGCTGGCTGTC 60
 QY 61 TCTGGTCCATCCGACGAGTGGTATTACTGGAGTTGGATCCGCGAGCTCAGGG 120
 DB |||||||
 61 TCTGGCGCTCCATCCGACGAGTGGTATTACTGGAGTTGGATCCGCGAGCTCAGGG 120
 QY 121 AAGGCGCTGGAGTGGATCGGTATCTATCACAGTGGCAACACTACAAACCCGCTCC 180
 DB |||||||
 121 AAGGCGCTGGAGTGGATCGGTATCTATCACAGTGGCAACACTACAAACCCGCTCC 180
 QY 181 CTCAAGAGTCAGTTACATGTCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGGCTG 240
 DB |||||||
 181 CTCAAGAGTCGAATTGCGATGCGGTAGACAGCTCTGAGAACAAGTTCTCCCTGAGGCTG 240
 QY 241 AGCTCTGTGACTCGCGGGACAGCGCGTATTACTGTGGAGTTCAGATGGGTACACT 300
 DB |||||||
 241 AACTCTGTGACTCGCGGGACAGCGCGTATTACTGTGGAGTTCAGATGGGTACACT 300
 QY 301 TTGGACAACCTGGGCGCAGGAACCCCTGGTCACCGCTCCCTCA 342
 DB |||||||
 301 TTGGACAACCTGGGCGCAGGAACCCCTGGTCACCGCTCCCTCA 342
 RESULT 4
 AF062112
 LOCUS 414 bp mRNA linear PRI 08-MAY-2001

DEFINITION Homo sapiens clone 2lu-26 immunoglobulin heavy chain variable
 region (IGH) mRNA, partial cds.
 ACCESSION AF062112
 VERSION AF062112.1 GI:3170686
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 414)
 AUTHORS Wang, X. and Stollar, B.D.
 TITLE Immunoglobulin VH gene expression in human aging
 JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)
 MEDLINE 93459182
 PUBMED 10527689
 REFERENCE 2 (bases 1 to 414)
 AUTHORS Wang, X. and Stollar, B.D.
 TITLE Direct Submission
 JOURNAL Submitted (22-APR-1998) Biochemistry Department, Tufts University
 School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
 FEATURES
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 1. .414
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 Best Local Similarity 90.0%; Pred. No. 9.9e-71;
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 QY 4 GAGTCTGGCCAGACCTGGTGAAGCTTACAGACCCCTGTCCTCAGCTGACTGTCTCT 63
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 73 GAGTGGGCCAGGACTGGTGAAGCTTACAGACCCCTGTCCTCAGCTGACTGTCTCT 132
 QY 64 GTGGGTCCATCCGACGAGTGGTGGTATTACTGGAGTTGGATCCGCCAGCTCCAGGGAAG 123
 DB |||||||
 133 GTGGGTCCATCAGCAGTGGTGATTACTACTGGAGTTGGATCCGCCAGCTCCAGGGAAG 192
 QY 124 GGCTGGAGTGGATCGGTATCATCTATCACAGTGGCAACACTTCTCCCTGAGGCTGAGC 183
 DB |||||||
 193 GGCTGGAGTGGATCGGTATCATCTATCACAGTGGCAACACTTCTCCCTGAGGCTGAGC 252
 QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
 DB |||||||
 253 AAGAGTCGAGTTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 312
 QY 244 TCTGTGACTGCCGCGACAGCGCGGTGTATTACTGTGCGAGGTCAGATGGGTACACTTTG 303
 DB |||||||
 313 TCTGTGACTGCCGCGACAGCGCGGTGTATTACTGTGCGGCTGGGTACACGAGCTGCTTT 372
 QY 304 GACAACTGGGGCCAGGGAACCTTGGTCACCGTCTCTCA 342

QY 304 GACAACTGGGGCCAGGAAACCTGGTCAACCGTCTCTCA 342
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 Db 316 GACTACTGGGGCCAGGAGCCCTGGTCAACCGTCTCTCA 354
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RESULT 9
 HSU80129 360 bp DNA linear PRI 19-FEB-1997
 DEFINITION Human immunoglobulin heavy chain variable region (V4-31) gene,
 partial cds.
 ACCESSION U80129
 VERSION U80129.1 GI:1791100
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.
 TITLE Analysis of rearranged immunoglobulin heavy chain variable region
 genes obtained from a bone marrow transplant (BMT) recipient
 Clin. Exp. Immunol. 107 (2), 372-380 (1997)
 JOURNAL
 MEDLINE 97182739
 PUBMED 9030878
 REFERENCE 2 (bases 1 to 360)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
 TITLE Direct Submission
 JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
 1000 Seneca Street, Seattle, WA 98101, USA
 FEATURES
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 /note="CD19+ peripheral blood B cells obtained from a bone
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 54 in reference 1"
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 /gene="V4-31"
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 /note="Ig VH4 heavy chain"
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 GWYFDYWGQGLTVTVSS"

ORIGIN

Query Match 82.7%; Score 283; DB 9; Length 360;
 Best Local Similarity 91.0%; Pred. No. 2.8e-70;
 Matches 314; Conservative 0; Mismatches 25; Indels 6; Gaps 1;
 QY 4 GAGTCTGCCCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCTCTCT 63
 Db 16 GAGTCGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCTCTCT 75
 QY 64 GTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTGGATCCGCGAGCGTCCAGGAG 123
 Db 76 GTGTGCTCCATCAGCAGTGGTGGTTATTACTGGAGTGGATCCGCGAGCGTCCAGGAG 135
 QY 124 GGCCTGGAGTGGATCGGTGATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
 Db 136 GGCCTGGAGTGGATCGGTGATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 195
 QY 184 AAGATCGAGTTACCATGTCACTAGACAGCTGTAGAACCACTTCTCCTGAGGCTGAGC 243

Db 196 AAGAGTCGAGTTACCATATCAGTAGACACAGCTTAAGAAACAGTTCTCCCTGAAGCTGAGC 255
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 QY 244 TCTGTGACTGGCGGACACGGCCGTGTATTACTGTGGAG-----GTCAGATGGGTAC 297
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 Db 256 TCTGTGACTGGCGGACACGGCCGTGTATTACTGTGGAGAGGGGTGAGTGGTGGTAC 315
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 QY 298 ACTTTGGCAACTGGGGCCAGGAAACCTGGTCAACCGTCTCTCTCA 342
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 Db 316 TATTTGACTACTGGGGCCAGGAAACCTGGTCAACCGTCTCTCTCA 360
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RESULT 10

HSU80130 360 bp DNA linear PRI 19-FEB-1997
 LOCUS Human immunoglobulin heavy chain variable region (V4-31) gene,
 partial cds.
 DEFINITION
 ACCESSION U80130
 VERSION U80130.1 GI:1791102
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 360)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.
 TITLE Analysis of rearranged immunoglobulin heavy chain variable region
 genes obtained from a bone marrow transplant (BMT) recipient
 Clin. Exp. Immunol. 107 (2), 372-380 (1997)
 JOURNAL
 MEDLINE 97182739
 PUBMED 9030878
 REFERENCE 2 (bases 1 to 360)
 AUTHORS Glas,A.M., Nottenburg,C. and Milner,E.C.B.
 TITLE Direct Submission
 JOURNAL Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
 1000 Seneca Street, Seattle, WA 98101, USA
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 /note="CD19+ peripheral blood B cells obtained from a bone
 marrow transplant recipient 1 year post transplant; clone
 55 in reference 1"
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 GWYFDYWGQGLTVTVSS"

ORIGIN

Query Match 82.7%; Score 283; DB 9; Length 360;
 Best Local Similarity 91.0%; Pred. No. 2.8e-70;
 Matches 314; Conservative 0; Mismatches 25; Indels 6; Gaps 1;
 QY 4 GAGTCTGCCCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCTCTCT 63
 Db 16 GAGTCGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCTCTCT 75
 QY 64 GTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTGGATCCGCGAGCGTCCAGGAG 123


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Db      76  GGTGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAG 135
Qy      124  GGCTGGAGTGGATCGGTACATCTATCAGTGSACACACTACAAACCCGTCCTC 183
Db      136  GGCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 195
Qy      184  AAGAGTCAGATTACCATGTCACTAGACAGCTTAAGAACCCTCTCTCCCTGAGGCTGAGC 243
Db      196  AAGAGTCAGATTACCATGTCACTAGACAGCTTAAGAACCCTCTCTCCCTGAGGCTGAGC 255
Qy      244  TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAG-----GTCAAGTGGGTAC 297
Db      256  TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGGGTGAGTGGCTGTAC 315
Qy      298  ACTTTGGACAACTGGGCGCAGGACCTGTCACCGTCTCTCA 342
Db      316  TATTTTGACTACTGGGGCAGGGAACCTGTGTCACCGTCTCTCA 360

RESULT 11
AF021954
LOCUS   Homo sapiens ID:CLL019 IgM heavy chain variable region mRNA,
DEFINITION partial cds.
ACCESSION AF021954
VERSION   AF021954.1
KEYWORDS  GI:3004697
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1. (bases 1 to 358)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     Differences in Ig variable region gene use and mutation in IgM vs
          IgG CLL suggest selection for distinct surface membrane Ig
          receptors
JOURNAL   Unpublished
REFERENCE 2. (bases 1 to 358)
AUTHORS   Chiorazzi, N.
TITLE     Direct Submission
JOURNAL   Submitted (02-SEP-1997) Medicine, North Shore University Hospital,
          350 Community Drive, Manhasset, NY 11030, USA
FEATURES  Location/Qualifiers
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          VTDFYWGQGLTVVSS"
CDS
Query Match 82.7%; Score 282.6; DB 9; Length 358;
Best Local Similarity 91.2%; Pred. No. 3.3e-70;
Matches 312; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy      4  GAGTCTGCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCA CCGTGCACCTGTCTCT 63
Db      16  GAGTGGGCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCA CCGTGCACCTGTCTCT 75
Qy      64  GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCGACGCTCCAGGGAAG 123
Db      76  GGTGCTCCATCAGCAGTGGTGGTTACTACTAGTGGAGCTGGATCCGCGACACCCAGGGAAG 135
Qy      124  GGCCTGGAGTGGATCGGCTGATATCTATCAGTGSACACACTACAAACCCGTCCTC 183

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Db      136  GGCCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 195
Qy      184  AAGAGTCAGATTACCATGTCACTAGTACACAGCTTAAGAACCCTCTCTCCCTGAGGCTGAGC 243
Db      196  AAGAGTCAGATTACCATGTCACTAGTACACAGCTTAAGAACCCTCTCTCCCTGAGGCTGAGC 255
Qy      244  TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGCTCAGAT---GGGTACACT 300
Db      256  TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAAGGGAGCTACGCTGACCCAC 315
Qy      301  TTGACAACTGGGCGCAGGGAACCTGTCACCGTCTCTCA 342
Db      316  TTTGACTACTGGGCGCAGGGAACCTGTGTCACCGTCTCTCA 357

RESULT 12
AF452917
LOCUS   Synthetic construct clone 7-161VH rotavirus VP7-specific antibody
DEFINITION heavy chain variable region mRNA, partial sequence.
ACCESSION AF452917
VERSION   AF452917.1
KEYWORDS  GI:25988060
SOURCE    synthetic construct
ORGANISM  synthetic construct
REFERENCE 1. (bases 1 to 403)
AUTHORS   Weitkamp, J.-H. and Crowe, J.E. Jr.
TITLE     Infant B Cell Repertoires are Sufficiently Diversified for Mature
          Virus-Specific Responses, but Lack Somatic Mutations
JOURNAL   Unpublished
REFERENCE 2. (bases 1 to 403)
AUTHORS   Weitkamp, J.-H. and Crowe, J.E. Jr.
TITLE     Direct Submission
JOURNAL   Submitted (28-NOV-2001) Pediatrics, Vanderbilt University Medical
          Center, 1161 21st Avenue South, D-7235 Medical Center North,
          Nashville, TN 37232-2581, USA
FEATURES  Location/Qualifiers
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          variable region"
ORIGIN
Query Match 82.4%; Score 281.8; DB 12; Length 403;
Best Local Similarity 91.2%; Pred. No. 6.3e-70;
Matches 311; Conservative 0; Mismatches 27; Indels 3; Gaps 1;

Qy      5  AGTCGCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCA CCGTGCACCTGTCTCTG 64
Db      42  AGTCGCCAGGACTGGTGAAGCCTTCA CAGACCCCTGTCCCTCA CCGTGCACCTGTCTCTG 101
Qy      65  GTGGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGGTCACGGGAAGG 124
Db      102  GTGGCTCCATCAGCAGTGGTGGTTATTACTGGAGTGGATCCGCCAGACCCAGGGAAG 161
Qy      125  GCCTGGAGTGGATCGGATCATCTATCACAGTGGCAACACCTACAAACCCGTCCTCA 184
Db      162  GCCTGGAGTGGATGGGTGATCATCTATTACAGTGGGAGCCTACTACAAACCCGTCCTCA 221
Qy      185  AGACTCAGATTACCATGTCACTAGTACACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGCT 244
Db      222  AGAGTCGAGTTACCATATCAGTACACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGCT 281
Qy      245  CTGTGACTGCCGCGGACACGCGCGTGTATTACTGTGG---AGTCAAGTGGGTACACTT 301

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Db      282 CTGTGACTCCGCGACACGCGCGTGTATTACTGTGCGAGCAGGTGGCTACGCGCCTGACT 341
QY      302 TGGACAACCTGGGCGAGGAACCCCTGGTCACCGTCTCCTCA 342
Db      342 TTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 382

RESULT 13
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LOCUS   HSA245020      351 bp      mRNA      linear      PRI 01-JUN-2000
DEFINITION Homo sapiens mRNA for immunoglobulin mu heavy chain variable region, partial, clone 2-E66.
ACCESSION AJ245020
VERSION   AJ245020.1 GI:4995498
KEYWORDS  IGM; Igm heavy chain; immunoglobulin mu heavy chain; variable region.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS   Dono, M., Zupo, S., Leanza, N., Melioli, G., Fogli, M., Melagrana, A., Chiorazzi, N. and Ferrarini, M.
          Heterogeneity of tonsillar subepithelial B lymphocytes, the splenic marginal zone equivalents
          J. Immunol. 164 (11), 5596-5604 (2000)
JOURNAL   20281644
MEDLINE   10820234
PUBMED    10820234
REFERENCE 2 (bases 1 to 351)
AUTHORS   Dono, M.
          Direct Submission
          Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunologia Clinica, L.go Rosanna benzi 10- Genova, ITALY
JOURNAL   1
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            Best Local Similarity 91.4%; Pred. No. 8.2e-70;
            Matches 310; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY      4 GAGTCGCGCCAGGACTGTGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACCTGTCTCT 63
Db      16 GAGTCGCGCCAGGACTGTGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACCTGTCTCT 75
QY      64 GGTGGCTCCATCCGACGTGGTGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db      76 GGTGGCTCCATCCGACGTGGTGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 135

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QY      124 GGCCTGGAGTGATCGGGTACATCTATCACAGTGGCAACACCTCAACAACCCGTCCTC 183
Db      136 GGCCTGGAGTGATGGGTGACATCTATTACAGTGGGAGCACCTACTACAACCGTCCCTC 195
QY      184 AAGAGTCGAGTTACCATGTCTAGTAGACACAGCTTAAGAACCATTCTCCCTGAGGCTGAGC 243
Db      196 AAGAGTCGAGTTACCATATCAGTAGACACAGCTCAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY      244 TCTGTGACTGCCGCGGACACGCGCTGTATTACTGTGAGGTCAAGTGGGTACACTTTG 303
Db      256 TCTGTGACTGCCGCGGACACGCGCTGTATTACTGTGCCAG--AGGGGGGTGGTCCGTT 312
QY      304 GACAACTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 342
Db      313 GACTACTGGGGCCAGGGAACCCCTGGTCACCGCTCTCCTCA 351

RESULT 14
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LOCUS     HST14X13      414 bp      mRNA      linear      PRI 30-APR-1997
DEFINITION H.sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone T14.13).
ACCESSION Z75365
VERSION   Z75365.1 GI:2062027
KEYWORDS  immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 414)
AUTHORS   Tonnelle, C., D'Ercole, C., Depraetere, V., Metras, D., Boubli, L. and Fougereau, M.
          Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?
          Int. Immunol. 9 (3), 407-414 (1997)
JOURNAL   9089979
MEDLINE   97244170
PUBMED    9089979
REFERENCE 2 (bases 1 to 414)
AUTHORS   Tonnelle, C.
          Direct Submission
          Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie Marseille Luminy, Marseille, 13288, France
JOURNAL   1
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            Best Local Similarity 90.9%; Pred. No. 1.8e-69;
            Matches 310; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

QY      4 GAGTCGCGCCAGGACTGTGTGAAGCCTTCACAGACCCCTGTCCTCACTGCACCTGTCTCT 63
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QY      64 GGTGGCTCCATCCGACGTGGTGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 123

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Db 133 GGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCCAGCAGCCAGGGAAG 192
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 Db 253 AAGAGTCGAGTTACCATGTCAGTAGACACGCTCTAAGAACCACTTCTCCCTCAGGCTGAGC 312
 Qy 244 TCTGTGACTGCCGGGACACGGCCGTGTATTACTGTGCGAGGTCA---GATGGGTACACT 300
 Db 313 TCTGTGACTGCCGGGACACGGCCGTGTATTACTGTGCGAGGTCAAGGGGTGTCCCTTAC 372
 Qy 301 TTGGACAACCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCCTC 341
 Db 373 TTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCCTC 413

RESULT 15
 HST14X4
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 DEFINITION H.sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone T14.4).
 ACCESSION Z75378
 VERSION Z75378.1 GI:2062042
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; variable region.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 414)
 Tonnelle,C., D'Ercole,C., Depraetere,V., Metras,D., Boubli,L. and Fougereau,M.
 Human thymic B cells largely overexpress the VH4 Ig gene family. A possible role in the control of tolerance in situ?
 Int. Immunol. 9 (3), 407-414 (1997)
 JOURNAL 97244170
 MEDLINE 9088979
 PUBLISHED
 REFERENCE 2 (bases 1 to 414)
 Tonnelle,C.
 Direct Submission
 AUTHORS
 TITLE Submitted (26-JUN-1996) Cecile Tonnelle, Centre d'Immunologie
 JOURNAL Marseille Luminy, Marseille, 13208, France
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 369. .414

Query Match 81.9%; Score 280.2; DB 9; Length 414;
 Best Local Similarity 90.9%; Pred. No. 1.8e-69;
 Matches 310; Conservative 0; Mismatches 28; Indels 3; Gaps 1;

Qy 4 GAGTCTGCCAGAGCTGGTGAAGCCTTTCAGACCCCTGTCCCTCAGCTGACTGTCTCT 63
 Db 73 GAGTCGGGCCCCAGGAGCTGGTGAAGCCTTTCAGACCCCTGTCCCTCAGCTGACTGTCTCT 132

Qy 64 GGTGGCTCCATCCGACGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCAGCTCAGGGAAG 123
 Db 133 GGTGGCTCCATCCGACGTGGTGGTTATTACTGGAGCTGGATCCGCCAGCAGCTCAGGGAAG 192
 Qy 124 GGCCTGGAGTGGATCGGGTACATCTATCACAAGTGGCAACACTACAAACCCCGTCCCTC 183
 Db 193 GGCCTGGAGTGGATCGGGTACATCTATCACAAGTGGGAGCACCTACTACAAACCCCGTCCCTC 252
 Qy 184 AAGAGTCGAGTTACCATGTCAGTAGACACGCTCTAAGAACCACTTCTCCCTCAGGCTGAGC 243
 Db 253 AAGAGTCGAGTTACCATGTCAGTAGACACGCTCTAAGAACCACTTCTCCCTCAGGCTGAGC 312
 Qy 244 TCTGTGACTGCCGGGACACGGCCGTGTATTACTGTGCGAGGTCA---GATGGGTACACT 300
 Db 313 TCTGTGACTGCCGGGACACGGCCGTGTATTACTGTGCGAGGTCAAGGGGTGTCCCTTAC 372
 Qy 301 TTGGACAACCTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCCTC 341
 Db 373 TTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCCTC 413

Search completed: August 13, 2004, 03:58:00
 Job time : 1472.46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 2005.71 seconds

(without alignments)

5091.898 Million cell updates/sec

Title: US-10-027-725A-3

Perfect score: 342

Sequence: 1 ctogactgtgccccaggact.....ccctgggtcacogtctctca 342

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpi:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	273.4	79.9	832	9	AU122174
2	264	77.2	607	12	BM783015
3	261.4	76.4	677	12	BM783015 K-EST0060
4	258.8	75.7	509	10	BM783015 K-EST0060 BG686767 602650737 AW406349 UI-HF-BL0

5	257.8	75.4	490	14	CD689564
6	256.6	75.0	369	10	AW404242
7	254	74.3	643	9	AU134293
8	252.6	73.9	1108	12	BM920469
9	250	73.1	977	13	BM920469 AGENCOURT
10	250	73.1	1201	13	BM920469 AGENCOURT
11	249.8	73.0	914	12	BM920469 AGENCOURT
12	248.4	72.6	890	13	BM920469 AGENCOURT
13	248	72.5	904	13	BM920469 AGENCOURT
14	246.4	72.0	447	10	AW402200
15	246.2	72.0	725	12	BM920469 AGENCOURT
16	246.2	72.0	959	13	BM920469 AGENCOURT
17	246	71.9	813	13	BM920469 AGENCOURT
18	245.8	71.9	582	10	AW401348
19	245.8	71.9	1050	9	AL552672
20	244.8	71.6	363	10	AW403420
21	244.6	71.5	903	13	BM920469 AGENCOURT
22	244.2	71.4	814	12	BM920469 AGENCOURT
23	244.2	71.4	828	10	BM920469 AGENCOURT
24	244	71.3	421	10	AW407630
25	243.8	71.3	856	13	BM920469 AGENCOURT
26	241.6	70.6	542	10	AW951834
27	241.6	70.6	1019	13	BM920469 AGENCOURT
28	241.6	70.6	1195	13	BM920469 AGENCOURT
29	241.4	70.6	474	10	AW408410
30	241.4	70.6	924	13	BM920469 AGENCOURT
31	240.6	70.4	368	10	AW403989
32	240.2	70.2	921	13	BM920469 AGENCOURT
33	240.2	70.2	939	13	BM920469 AGENCOURT
34	239.8	70.1	915	13	BM920469 AGENCOURT
35	239.8	70.1	1201	13	BM920469 AGENCOURT
36	239.4	70.0	924	12	BM920469 AGENCOURT
37	239.4	70.0	942	13	BM920469 AGENCOURT
38	239.4	70.0	1201	13	BM920469 AGENCOURT
39	239.2	69.9	856	12	BM920469 AGENCOURT
40	238.6	69.8	357	12	BM920469 AGENCOURT
41	238.6	69.8	548	10	AW402602
42	238.6	69.8	661	12	BM920469 AGENCOURT
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44	238.4	69.7	923	13	BM920469 AGENCOURT
45	238.4	69.7	928	13	BM920469 AGENCOURT

ALIGNMENTS

RESULT 1
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LOCUS AU122174 MAMMAL Homo sapiens cdna clone MAMMAL001802 5', mRNA
DEFINITION AU122174 MAMMAL Homo sapiens cdna clone MAMMAL001802 5', mRNA
ACCESSION AU122174
VERSION AU122174.1 GI:10937409
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project: 5' - & 3' - end one pass sequencing: Helix Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
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/clone="MAMMA1001802"
/tissue_type="mammary gland"
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/note="Vector: pME18SFL3"

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Best Local Similarity 87.9%; Pred. No. 8.2e-62;
Matches 298; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 63
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QY 124 GGCCTGGAGTGATCGGTACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
DB 230 GGCCTGGAGTGATCGGTACATCTATTAATGGGAACCTTACTACAAACCCGTCCTC 289

QY 184 AAGAGTCGAGTTACCATGTGCTAGACAGCTCTAAGAACCCTTCTCCCTGAGGTGAGC 243
DB 290 AAGAGTCGAGTTACCATGTGCTAGACAGCTCTAAGAACCCTTCTCCCTGAGGTGAGC 349

QY 244 TCTGTGACTGCGCGGACACGGCCGTTATTACTGTGGAGTTCAGATGGGTACACTTTG 303
DB 350 TCTGTGACTGCGCGGACACGGCCGTTATTACTGTGGAGTTCAGATGGGTACACTTTG 409

QY 304 GACAACTGGGCGCAGGACCTGTGCACCGTCTCTCA 342
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RESULT 2
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LOCUS K-EST0060735 S18N669761 Homo sapiens cDNA clone S18N669761-2-E06
DEFINITION 5', mRNA sequence.

ACCESSION BM783015
VERSION BM783015.1 GI:19131247
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 607)

Kim N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yusong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 2 row: E column: 06

High quality sequence stop: 607.

Location/Qualifiers

1..607

/organism="Homo sapiens"

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FEATURES

source

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/sex="p"

/lab_host="Top10P"

/clone_lib="S18N669761"

/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10P, by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 77.2%; Score 264; DB 12; Length 607;
Best Local Similarity 87.4%; Pred. No. 2.2e-59;
Matches 304; Conservative 0; Mismatches 35; Indels 9; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 63
DB 112 GAGTGGGCCAGGACTGGTGAAGCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 171

QY 64 GGTGCTCATCCGACGTGGTGGTTATTACTGGAGTTGGATCGCCAGGCTCCAGGGAAG 123
DB 172 GGTGCTCATCGAAGCAGTGGTAGTTACTGGAGTGGATCGCCCAACACCCAGGGAAG 231

QY 124 GGCCTGGAGTGATCGGTACATCTATCACAGTGGCAACACCTACAAACCCGTCCTC 183
DB 232 GGCCTGGAGTGATCGGTACATCTATCACAGTGGGAGCACCTACTACAAACCCGTCCTC 291

QY 184 AAGAGTCGAGTTACCATGTGCTAGACAGCTCTAAGAACCCTTCTCCCTGAGGTGAGC 243
DB 292 AAGAGTCGAGTTACCATGTGCTAGACAGCTCTAAGAACCCTTCTCCCTGAGGTGAGC 351

QY 244 TCTGTGACTGCGCGGACACGGCCGTTATTACTGTGGAG-----GTGAGTGGG 294
DB 352 TCTGTGACTGCGCGGACACGGCCGTTATTACTGTGGAGAGATGGCAATTACGATAAT 411

QY 295 TACACTTTGGACAACTGGGGCCAGGAAACCTGTGCACCGTCTCTCTCA 342
DB 412 TACGGTATGGAGCTGTGGGGCCAGGACCCGTCACCGTCTCTCTCA 459

RESULT 3

BM786767

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BM786767 677 bp mRNA linear EST 01-MAY-2001
602650737F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763217 5',
mRNA sequence.

BM786767

BM786767.1 GI:13918164

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 677)

NIH-MGC <http://mgs.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1CM1618 row: i column: 10
High quality sequence stop: 675.
Location/Qualifiers
1. 677
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/db_xref="taxon:9606"
/clone="IMAGE:4763217"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
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/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES
source

ORIGIN

Query Match 76.4%; Score 261.4; DB 12; Length 677;
Best Local Similarity 89.0%; Pred. No. 1.1e-58;
Matches 307; Conservative 0; Mismatches 31; Indels 7; Gaps 2;
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Qy 99 GAGTCGGGCCAGCACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCT 158
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Db |||||
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Db |||||
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Db |||||
Qy 218 GGCTGGAGTGGATGGGTACATCTATTACAGTGGGAGCACCTACTACAAACCCGTCCTC 277
Db |||||
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Db |||||
Qy 278 AAGAGTCGAATTACCATATCAGTACAGACGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 337
Db |||||
Qy 244 TCTGTGACTGCCGGGACACGCCGCTGATTACTGTGCGA-----GGTCAGATGGGTAC 297
Db |||||
Qy 338 TCTGTGACTGCCGGGACACGCCGCTGATTACTGTGCGAGATCGCAAGAGAGGAGGC 397
Db |||||
Qy 298 ACTTTGGACACTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 342
Db |||||
Qy 398 GGGTTCGACCCCTGGGGCCAGGGAACCTGTGTCACCGTCTCTCTCA 442
Db |||||

RESULT 4
AW406349
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DEFINITION UI-HF-BLO-aco-h-03-0-UT.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059933 5', mRNA sequence.
AW406349
ACCESSION
VERSION AW406349.1 GI:6925406
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 509)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
TITLE
AUTHORS
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov/bbrp/image/image.html>
Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
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/note="vector: p77T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 75.7%; Score 258.8; DB 10; Length 509;
Best Local Similarity 86.8%; Pred. No. 4.7e-58;
Matches 297; Conservative 0; Mismatches 42; Indels 3; Gaps 1;
Qy 4 GAGTCTGCCAGCACTGGTGAAGCCTTCACAGACCCCTGCTCCCTCAGCTGCTCTCT 63
Db |||||
Qy 54 GAGTCGGGCCAGCACTGGTGAAGCCTTCGAGACCCCTGCTCCCTCAGCTGCTCTCT 113
Db |||||
Qy 64 GGTGGCTCCATCCGACGAGTGGTATTACTGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db |||||
Qy 114 GGTGGCTCCATCAGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 173
Db |||||
Qy 124 GGCTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTACACAAACCCGTCCTC 183
Db |||||
Qy 174 GGCTGGAGTGGATGGGAGTATCTATTATAGTGGGAGCACCTACTACAAACCCGTCCTC 233
Db |||||
Qy 184 AAGAGTCGAGTTACCATGTCAGTACAGACGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db |||||
Qy 234 AAGAGTCGAGTCCACATATCAGTAGACACGCTCCAGAACCACTTCTCCCTGAGGCTGAGC 293
Db |||||
Qy 244 TCTGTGACTGCCGGGACACGCCGCTGATTACTGTGCGAG-----GTGAGATGGGTACT 300
Db |||||
Qy 294 TCTGTGACCCGCGGACACGCCGCTGATTACTGTGCGAGACCCCTCTCTACGAGACCTGG 353
Db |||||
Qy 301 TTGGACAACCTGGGCCAGGGAACCCCTGTCAACCGTCTCTCTCA 342
Db |||||
Qy 354 TTCGACCCCTGGGGCCAGGGAACCCCTGTCAACCGTCTCTCTCA 395
Db |||||

RESULT 5
CD689564
LOCUS
DEFINITION EST6087 human nasopharynx Homo sapiens cDNA, mRNA sequence.
CD689564
ACCESSION
VERSION CD689564.1 GI:32209443
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
Transcriptional Gene Expression Profile of Human Nasopharynx
Unpublished (2003)
TITLE
JOURNAL
COMMENT Contact: Yixin Zeng

Cancer Center
Sun Yat-sen University
651 DongFeng Road East, Guangzhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@zsums.edu.cn.

FEATURES
Location/Qualifiers
1. 490

/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 75.4%; Score 257.8; DB 14; Length 490;
Best Local Similarity 86.8%; Pred. No. 8.6e-58;
Matches 296; Conservative 0; Mismatches 42; Indels 3; Gaps 1;
QY 5 AGCTCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTCG 64
DB 111 AGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTCG 170
QY 65 GTGGGTCCATCCGACGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGCTCCAGGAAGG 124
DB 171 GTGACTCCATCAGCAGTGTGGTTACTACTGAGTTGGATTGCCAGCACCCAGGAAGG 230
QY 125 GCCTGGAGTGGATCGGGTACATCTATCAAGTGGCAACACCTPACAAACCCGTCCTCA 184
DB 231 GCCTCGAGTGGATGGGTACATCTATCAAGTGGGAGTGCAGACTACACCCGTCCTCA 290
QY 185 AGAGTCGAGTACCATGTCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGCT 244
DB 291 AGAGTCGAGTACCATGTCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGGT 350
QY 245 CTGTGACTGCCCGGACACGGCGGTGTTATTACTGTGGAGGTTCAGAT---GGGTACACTT 301
DB 351 CTGTGACGGCGGACACGGCGGTGTTATTACTGTGGAGGTTCAGAT---GGGTACACTTAA 410
QY 302 TGGACAACATGGGGCAGGGAACCTGGTCAACCTGTCCTCA 342
DB 411 TTGACTACTGGGGCAGGGAATCCTGGTCACCGTCTCCTCA 451

RESULT 6

AW404242
LOCUS
DEFINITION
UI-HF-BLO-abq-f-09-0-UI.r1 NIH_MGC 37 Homo sapiens cDNA clone
IMAGE:3057545 5', mRNA sequence.

ACCESSION
AW404242.1 GI:6923299

VERSION
EST.

KEYWORDS
SOURCE

ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 369)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

DNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL.at:

www.bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
1. 369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3057545"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonald, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 75.0%; Score 256.6; DB 10; Length 369;
Best Local Similarity 87.8%; Pred. No. 1.5e-57;
Matches 280; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCT 63
DB 34 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCT 93
QY 64 GGTGGCTCCATCCGACGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGAAG 123
DB 94 GGTGGCTCCATCCGACGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGAAG 153
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAAGTGGCAACACCTTACAAACCCGTCCTTC 183
DB 154 GGCCTGGAGTGGATCGGGTACATCTATCAAGTGGGAGCACCTTACAAACCCGTCCTTC 213
QY 184 AGAGTCGAGTACCATGTCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 214 AGAGTCGAGTACCATGTCTAGTAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 273
QY 244 TCTGTGACTGCCCGGACACGGCGGTGTTATTACTGTGGAGGTTCAGATGGGTACACTTTG 303
DB 274 TCTGTGACTGCCCGGACACGGCGGTGTTATTACTGTGGAGGTTCAGATGGGTACACTTT 333
QY 304 GACAACTGGGGCCAGGGAA 322
DB 334 GATAGTAGTGGTTACGGAA 352

RESULT 7

AUI34293

LOCUS

DEFINITION

AUI34293 OVARC1 Homo sapiens cDNA clone OVARC1001672 5', mRNA

sequence.

ACCESSION

AUI34293.1 GI:10994832

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 643)

Ota.T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,

Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and

Isogai,T.

HRI human cDNA project

Unpublished (2000)

Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute

FEATURES

Location/Qualifiers

1..643

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="OVARC1001672"

/tissue_type="ovary, tumor tissue"

/clone_lib="OVARC1"

/note="Vector: pME18SFL3"

ORIGIN

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Query Match      74.3%; Score 254; DB 9; Length 643;
Best Local Similarity 85.1%; Pred. No. 1e-56;
Matches 303; Conservative 0; Mismatches 35; Indels 18; Gaps 1;

QY 5 AGTCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCTG 64
   |||||
Db 110 AGTCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCTG 169

QY 65 GTGGCTCATCCGAGTGGTGTTATTACTGGAGTTGGATCCGCGAGGTCACAGGAAG 124
   |||||
Db 170 GTGGCTCATCCGAGTGGTGTTATTACTGGAGTTGGATCCGCGAGGTCACAGGAAG 229

QY 125 GCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACACCTACACACCGTCCCTCA 184
   |||||
Db 230 GCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACACCTACACACCGTCCCTCA 289

QY 185 AGAGTCGAGTTACCATGTGCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGCT 244
   |||||
Db 290 AGAGTCGAGTTACCATGTGCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGG 349

QY 245 CTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGTGCAGAGTGCAGTACACT---- 300
   |||||
Db 350 CTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGTGCAGAGTGCAGTACACT---- 409

QY 301 -----TTTGACAACTGGGCGGAGGACCCCTGTGTCACCTGTCCTCA 342
   |||||
Db 410 GGACCTACAGTAAGTTGACCACCTGGGCGGAGGAAACCCGTGTCACCTGTCCTCA 465

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RESULT 8
BM920469
LOCUS BM920469
DEFINITION AGENCOURT_6709612 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5750444
5', mRNA sequence.
ACCESSION BM920469
VERSION BM920469.1 GI:19370848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12781 row: g column: 21
High quality sequence stop: 626.
Location/Qualifiers
1..1108
/organism="Homo sapiens"

```

FEATURES

Location/Qualifiers

1..1108

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5750444"

/lab_host="DH10B"

/clone_lib="NIH_MGC_122"

Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed, and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

ORIGIN

```

Query Match      73.9%; Score 252.6; DB 12; Length 1108;
Best Local Similarity 85.5%; Pred. No. 3.2e-56;
Matches 295; Conservative 0; Mismatches 44; Indels 6; Gaps 1;

QY 4 GAGTCGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACCTGTCTCT 63
   |||||
Db 110 GAGTCGCGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGCACCTGTCTCT 169

QY 64 GGTGCTCCATCCGAGTGGTGGTATTACTGGAGTTGGATCCGCGAGGTCACAGGAAG 123
   |||||
Db 170 GGTGCTCCGTCAGCAGTGGTAGTTACTACTGGAGTGGATCCGCGAGGTCACAGGAAG 229

QY 124 GGCCTGGAGTGGATCGGGGTACATCTATCACAGTGGCAACACTACAAACCCGTCCTCA 183
   |||||
Db 230 GGCCTGGAGTGGATCGGGGTATATCTATTACAGTGGGAGCACCACTACACCCCTCCCTC 289

QY 184 AAGAGTCGAGTTACCATGTGCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
   |||||
Db 290 AAGAGTCGAGTTACCATGTGCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 349

QY 244 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGTGCAGTGGG-----TAC 297
   |||||
Db 350 TCTGTGACTGCGCGGACACGGCCGTGTATTACTGTGCGAGTGCAGTGGGCGGCGGACTAC 409

QY 298 ACTTTGGACAACTGGGCGGAGGAAACCTGTGTCACCTGTCCTCA 342
   |||||
Db 410 TACATGACGCTCTGGGCGCAAGGGACCGTCAACCGTCTCTCA 454

```

```

RESULT 9
BX396901
LOCUS BX396901
DEFINITION BX396901 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI026YB08 5-PRIME, mRNA sequence.
ACCESSION BX396901
VERSION BX396901.1 GI:30625036
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 977)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI026B04QPI&cluster=7198.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

```

Faraday Avenue Genoscope sequence ID : CS0DI026BC04QP1.

FEATURES
source

1..977
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI026YR08"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 73.1%; Score 250; DB 13; Length 977;
Best Local Similarity 84.5%; Pred. No. 1.5e-55;
Matches 299; Conservative 0; Mismatches 40; Indels 15; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 63
Db 163 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 222
QY 64 GGTGGCTCCATCGCAGTGGTGTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 123
Db 223 GGTGGCTCCATCAGCAGTGGTGTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 282
QY 124 GGCCTGGAGTGGATCGGTACATCTATCAGCTGGCAACACCTACAGAACCCGCTCCCTC 183
Db 283 GGAAGTGGAGTGGATCGGTGTCTATACAGTGGGAGCACCACCACTACCAACCCCTCCCTC 342
QY 184 AAGAGTCGAGTTACCACTGTCAGTAGACAGTCTAAGAACCACTTCCTCCCTGAGGCTGAGC 243
Db 343 AAGAGTCGAGTTACCACTGTCAGTAGACAGTCTAAGAACCACTTCCTCCCTGAGGCTGAGC 402
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGA-----GGTCA 288
Db 403 TCTGTGACCGCGCAGACACGCGCGTGTATTACTGTGCGATCACCAGCATAGTGGCTAC 462
QY 289 GATGGGTACACTTTGGACACTGGGGCCAGGAAACCTGGTCAACCGTCTCCTCA 342
Db 463 GATGAGGGTGTGTTGACTACTGGGGCCAGGAAACCTGGTCAACCGTCTCCTCA 516

RESULT 10

BX336959
LOCUS
DEFINITION
BX336959 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI034YI02 5-PRIME, mRNA sequence.
BX336959
ACCESSION
BX336959.1 GI:30341572
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7198.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI034BE01QP1&cluster=7198.r. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI034BE01QP1.

FEATURES

source

1..1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI034YI02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 73.1%; Score 250; DB 13; Length 1201;
Best Local Similarity 84.5%; Pred. No. 1.7e-55;
Matches 299; Conservative 0; Mismatches 40; Indels 15; Gaps 1;
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 63
Db 156 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 215
QY 64 GGTGGCTCCATCGCAGTGGTGTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 123
Db 216 GGTGGCTCCATCAGCAGTGGTGTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 275
QY 124 GGCCTGGAGTGGATCGGTACATCTATCAGCTGGCAACACCTACAGAACCCGCTCCCTC 183
Db 276 GGAAGTGGAGTGGATCGGTGTCTATACAGTGGGAGCACCACCACTACCAACCCCTCCCTC 335
QY 184 AAGAGTCGAGTTACCACTGTCAGTAGACAGTCTAAGAACCACTTCCTCCCTGAGGCTGAGC 243
Db 336 AAGAGTCGAGTTACCACTGTCAGTAGACAGTCTAAGAACCACTTCCTCCCTGAGGCTGAGC 395
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGA-----GGTCA 288
Db 396 TCTGTGACCGCGCAGACACGCGCGTGTATTACTGTGCGATCACCAGCATAGTGGCTAC 455
QY 289 GATGGGTACACTTTGGACAACTGGGGCCAGGAAACCTGGTCAACCGTCTCCTCA 342
Db 456 GATGAGGGTGTGTTGACTACTGGGGCCAGGAAACCTGGTCAACCGTCTCCTCA 509

RESULT 11

BG757054
LOCUS
DEFINITION
BG757054 NTH_MGC_48 Homo sapiens cDNA clone IMAGE:4850851 5', mRNA sequence.
BG757054
ACCESSION
BG757054.1 GI:14067707
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 914)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1692 row: 1 column: 20
High quality sequence stop: 854.

FEATURES

source
1..914
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
 /clone="IMAGE:4850851"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected 500bp
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.0%; Score 249.8; DB 12; Length 914;
 Best Local Similarity 86.7%; Pred. No. 1.6e-55;
 Matches 301; Conservative 0; Mismatches 37; Indels 9; Gaps 2;
 QY 4 GAGCTGGCCGACGACTGGTGAAGCCTTCACAGACCCCTGCCCTCAGCTGACTGTCTCT 63
 Db 93 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCCCTCAGCTGACTGTCTCT 152
 QY 64 GGTGGCTCCATCCCGCAGTGGTGGTTATTACTGGAGTTGGATCCGCGCAGCGTCCAGGGAAG 123
 Db 153 GGTGGCTCCATCAGCAGTGGTGGTTATTACTGGAGTTGGATCCGCGCAGCGTCCAGGGAAG 211
 QY 124 GGCCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTTCAACAACCCCGTCCCTC 183
 Db 212 GGCCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTTCAACAACCCCGTCCCTC 271
 QY 184 AAGAGTCAGTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 243
 Db 272 AAGAGTCAGTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 331
 QY 244 TCTGTGACTCGCGGACACGCGCGTGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 303
 Db 332 TCTGTGACTCGCGGACACGCGCGTGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 391
 QY 304 GACAACT-----GGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 342
 Db 392 CACGACTTGACTACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 438

RESULT 12

BX324929
 LOCUS BX324929 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0DI086YJ13 5-PRIME, mRNA sequence.
 ACCESSION BX324929
 VERSION BX324929.1 GI:30338413
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 890)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 7198.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0AI086CE07QPI&cluster=7198.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0AI086CE07QPI.

FEATURES
 source

Location/Qualifiers
 1..890
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI086YJ13"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 72.6%; Score 248.4; DB 13; Length 890;
 Best Local Similarity 84.2%; Pred. No. 3.7e-55;
 Matches 298; Conservative 0; Mismatches 41; Indels 15; Gaps 1;
 QY 4 GAGTCTGGCCGACGACTGGTGAAGCCTTCACAGACCCCTGCCCTCAGCTGACTGTCTCT 63
 Db 133 GAGTGGGGCCAGGACTGGTGAAGCCTTCGAGACCCCTGTCCTCAGCTGACTGTCTCT 192
 QY 64 GGTGGCTCCATCCCGCAGTGGTGGTTATTACTGGAGTTGGATCCGCGCAGCGTCCAGGGAAG 123
 Db 193 GGTGGCTCCATCAGCAGTGGTGGTTATTACTGGAGTTGGATCCGCGCAGCGTCCAGGGAAG 252
 QY 124 GGCCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTTCAACAACCCCGTCCCTC 183
 Db 253 GGCCTGAGTGGATCGGGTACATCTATCAGAGTGGCAACACCTTCAACAACCCCGTCCCTC 312
 QY 184 AAGAGTCAGTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 243
 Db 313 AAGAGTCAGTACCATGTCTAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGCTGAGC 372
 QY 244 TCTGTGACTCGCGGACACGCGCGTGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 293
 Db 373 TCTGTGACTCGCGGACACGCGCGTGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 432
 QY 294 -----GTACACTTTGGACAACCTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 342
 Db 433 TGCTACCTCGCCTTTGACTACTGGGGCCAGGGAACCCCTGGTCAACGCTCTCTCA 486

RESULT 13

BQ710488
 LOCUS BQ710488 904 bp mRNA linear EST 16-JUL-2002
 DEFINITION AGENCOURT 8352970 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278137
 5', mRNA sequence.
 ACCESSION BQ710488
 VERSION BQ710488.1 GI:21849387
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 904)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: Agencourt Bioscience Corporation
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LICM2465 row: k column: 02
 High quality sequence stop: 728.
 Location/Qualifiers
 1..904
 /organism="Homo sapiens"

FEATURES
 source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6278137"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match      72.5%; Score 248; DB 13; Length 904;
Best Local Similarity 84.5%; Pred. No. 4.8e-55;
Matches 294; Conservative 0; Mismatches 45; Indels 9; Gaps 1;

QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTCTCTCT 63
DB 86 GAGTCTGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCACCTGCACCTCTCTCT 145
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
DB 146 GGTGCTCCATCAGCAGTAGTATTACTACTGGGCTGGATCCGCGAGCGCCCGAGGGAAG 205
QY 124 GGCCTGGAGTGGATCGGCTACATCTATCAGCTGCGACACCTACACACCCGTCCTCTC 183
DB 206 GGGCTGGAGTGGATGGGAGTATCTATTATAGTGGAGCACCTACTACACCCGTCCTCTC 265
QY 184 AAGAGTCGAGTTACCATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 266 AAGAGTCGAGTCACCATATCCGTAGACAGCTCCAGAACCACTTCTCCCTGAGGCTGAGC 325
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAGTCTAGA-----TGGG 294
DB 326 TCTGTGACCGCGGACACGCGCTGTATTACTGTGGAGACGAGCAGCAGCTGGTA 385
QY 295 TACACTTTGGACACTGGGCGGAGGACCCCTGTGTCACCGTCTCTCTCA 342
DB 386 CATTACTTCCAGCATGGGCGGAGGCGACCCCTGGTCAACGCTCTCTCTCA 433

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RESULT 14

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AW402200
LOCUS      UI-HF-BKO-aat-d-09-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
DEFINITION IMAGE:3054785 5', mRNA sequence.
ACCESSION AW402200
VERSION    AW402200.1 GI:6920886
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
Location/Qualifiers
1..447

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FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3054785"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_36"
/note="Vector: pT73-Pac; Site 1: NotI; Site 2: EcoRI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

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ORIGIN

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Query Match      72.0%; Score 246.4; DB 10; Length 447;
Best Local Similarity 84.2%; Pred. No. 8.7e-55;
Matches 293; Conservative 0; Mismatches 46; Indels 9; Gaps 1;

QY 4 GAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTCTCTCT 63
DB 47 GAGTCTGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCTCTCTCTCTCTCTCTCT 106
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
DB 107 GGTGCTCCATCAGCAGGAGTAGTATTACTTGGGCTGGATCCGCGAGCGCCCGAGGGAAG 166
QY 124 GGCCTGGAGTGGATCGGCTACATCTATCAGCTGCGACACCTACACACCCGTCCTCTC 183
DB 167 GGGCTGGAGTGGATGGGAGTATCTATTATAGTGGAGCACCTACTACACCCGTCCTCTC 226
QY 184 AAGAGTCGAGTTACCATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 227 AAGAGTCGAGTCACCATATCAATAGACACGCTCCAGAACCACTTCTCTCTGAGGCTGAGC 286
QY 244 TCTGTGACTGCGCGGACACGCGCTGTATTACTGTGGAG-----GTCAGATGGG 294
DB 287 TCTGTGACCGCGGACACGCGCTGTATTACTGTGGAGAGGAGGATGGTGTATGCT 346
QY 295 TACACTTTGGACACTGGGCGGAGGACCCCTGTGTCACCGTCTCTCTCA 342
DB 347 CACTGGTTCCAGCCCTGGGCGGAGGGAACCTGGTCAACGCTCTCTCTCA 394

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RESULT 15

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BG431274
LOCUS      602499844F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4613435 5',
DEFINITION mRNA sequence.
ACCESSION BG431274
VERSION    BG431274.1 GI:13337780
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 725)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1363 row: h column: 12
High quality sequence stop: 716.
Location/Qualifiers

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FEATURES

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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4613435"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NIH MGC 75"
            /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site:1;
            SfiI (ggccattatggcc); Site:2: SfiI (ggccattatggcc); 5' and
            3' adaptors were used in cloning as follows: 5' adaptor
            sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
            5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.65
            kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA). Note: this is a NIH MGC Library."

ORIGIN
Query Match      72.0%; Score 246.2; DB 12; Length 725;
Best Local Similarity 82.9%; Pred. No. 1.3e-54;
Matches 281; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy      4  GAGTCTGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGCTCTCT 63
Db      109 GAGTCGGGCCCAAGACTGGTGAAGCCTTCGGGGACCCCTGTCCTCACCTGCACCTGCTCTCT 168

Qy      64  GGTGGCTCCATCCGGCAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGGAAG 123
Db      169 GGTGGCTCCATCCATCAGTCCCATTTATTACTGGGGCTGGATCCGCCAGCCGCCAGGGGAAG 228

Qy      124 GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACCTACACACCCCGTCCCTC 183
Db      229 GGGCTGGAGTGGATTGCCAGTATCTCTCACAGTGGGACCACTACTACACCCCGTCCCTC 288

Qy      184 AAGAGTCGAGTTACCATGTCACTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db      289 GAGAGTCGAGTCACCATATCCGTAGACACGTCCTAAGAACCACTTCTCCCTGAGGCTGAGG 348

Qy      244 TCTGTGACTGCGCGGAGACACGGCCGTGTATTACTGTGCGAGGTGAGATGGGTACACTTTG 303
Db      349 CCTGTGACCGCCGCGAGACACGCTCTGTATATTATTGTGCGAGATTACTCGGGGGGAGTTT 408

Qy      304 GACAACTGGGGCCAGGGAAACCCCTGGTCAACCGTCTCCTCA 342
Db      409 GACTATTGGGGCCAGGGAAACCCCTGGTCCGCTCTCCTCA 447
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Search completed: August 13, 2004, 07:13:20
Job time : 2006.71 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 222.818 Seconds

(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725A-3

Perfect score: 342

Sequence: 1 ctgagctcggccaggact.....ccctggctcaccgtctctctca 342

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	338.8	99.1	342	6	ABK89639 DNA encod
2	322.8	94.4	342	6	ABK89638 DNA encod
3	308.4	90.2	342	6	ABK89637 DNA encod
4	284.6	83.2	352	9	ADC99786 Anti-huma
5	284.6	83.2	352	9	ADD05390 Anti-MUC1
6	284.4	83.2	360	4	Aaf29076 Human HIV
7	275	80.4	352	9	ADC99778 Anti-huma
8	275	80.4	352	9	ADD05382 Anti-MUC1
9	273.8	80.1	369	4	Aaf29046 Human HIV
10	268.4	78.5	358	9	ADC99798 Anti-huma
11	268.4	78.5	358	9	ADD05402 Anti-MUC1
12	267.2	78.1	516	3	AAA46876 DNA encod
13	264	77.2	366	4	Aaf29066 Human HIV
14	263.6	77.1	357	2	AAQ38670 MAB GAH v
15	262.8	76.8	352	9	ADC99806 Anti-huma
16	262.8	76.8	352	9	ADD05410 Anti-MUC1
17	261.4	76.4	741	3	Aaz28998 Anti-muri
18	258.6	75.6	1644	2	Aaz24434 Human bla
19	257	75.1	324	4	ABS46332 Human liv
20	257	75.1	340	6	ABK84446 Human cDN
21	257	75.1	340	7	ACA64884 Human Ig
22	257	75.1	631	2	AAQ78969 Human imm
23	255.8	74.8	450	2	AAX90024 Human mon

ALIGNMENTS

RESULT 1

ABK89639
ID ABK89639 standard; DNA; 342 BP.

XX AC ABK89639;

XX DT 21-OCT-2002 (first entry)

XX DE DNA encoding human IgE Fab clone 100 heavy chain.

XX KW Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;

XX KW Timothy grass pollen allergen; passive immunotherapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..342

FT FT /*tag= a

FT FT /product= "Fab clone 100 heavy chain"

FT FT /*tag= b

FT FT /note= "PR1 region"

FT FT /*tag= c

FT FT /note= "CDR1 region"

FT FT /*tag= d

FT FT /note= "PR2 region"

FT FT /*tag= e

FT FT /note= "PR3 region"

FT FT /*tag= f

FT FT /note= "CDR2 region"

FT FT /*tag= g

FT FT /note= "PR3 region"

FT FT /*tag= h

FT FT /note= "CDR3 region"

FT FT /*tag= i

FT FT /note= "PR4 region"

WO200253595-A1.

XX

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PD 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI; 2002-583604/62.
XX P-PSDB; ABG30447.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX variable region of group 2 allergen specific-human IgE Fabs, useful for
XX diagnosing or passive immunotherapy of type I allergy, for environmental
XX allergen detection.
XX
XX Disclosure; Page 33; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human IgE Fabs and methods for their use. The proteins
XX of the invention may have anti-allergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX 2 allergen-specific fabs of the invention may be useful for environmental
XX allergen detection and for standardisation of allergen extracts. The fabs
XX - or a vaccine against a type I allergy is useful for passive
XX immunotherapy of type I allergy, it is also useful for diagnosing a type
XX I allergy. The allergen-specific fabs of the invention are useful for
XX inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX also useful for blocking the binding of grass pollen allergic patients
XX IgE antibodies to Phi P 2. The present sequence represents the DNA
XX encoding the human IgG fab, clone 100 heavy chain protein of the
XX invention
XX
XX Sequence 342 BP; 69 A; 103 C; 94 G; 76 T; 0 U; 0 Other;
XX
Query Match 99.1%; Score 338.8; DB 6; Length 342;
Best Local Similarity 99.4%; Pred. No. 1.1e-85;
Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTCTCCCTCACTGCCTGTC 60
DB 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTCTCCCTCACTGCCTGTC 60
OY 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGGCAGCGTCCAGGG 120
DB 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGGCAGCGTCCAGGG 120
OY 121 RAGGCGCTGGAGTGGGTACATCTATCATCAGTGGCAACCTACACACCGCTCC 180
DB 121 RAGGCGCTGGAGTGGGTACATCTATCATCAGTGGCAACCTACACACCGCTCC 180
OY 181 CTCAGAGTTCGAGTTACCATGTCAGTACACAGCTTAAGAACCTCTCCCTGAGGCTG 240
DB 181 CTCAGAGTTCGAGTTACCATGTCAGTACACAGCTTAAGAACCTCTCCCTGAGGCTG 240
OY 241 AGCTCTGTGACTGCGCGGACACCGGCGGTGTTATTCTGTGCGAGGTTCAGATGGGTACT 300
DB 241 AGCTCTGTGACTGCGCGGACACCGGCGGTGTTATTCTGTGCGAGGTTCAGATGGGTACT 300
OY 301 TTGGACAACCTGGGCGGACCGCTGGTCAACCGCTCTCTCA 342
DB 301 TTGGACAACCTGGGCGGACCGCTGGTCAACCGCTCTCTCA 342
RESULT 2
ABK89638
ID ABK89638 standard; DNA; 342 BP.
XX
XX AC ABK89638;
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XX
XX 21-OCT-2002 (first entry)
XX
XX DNA encoding human IgE Fab clone 60 heavy chain.
XX
XX Human; fab; ds; gene; anti-allergic; vaccine; grass pollen; Phi p 2;
XX timothy grass pollen allergen; passive immunotherapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
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XX FT misc_feature 7..78
XX FT /*tag= b
XX FT /note= "FR1 region"
XX FT misc_feature 79..99
XX FT /*tag= c
XX FT /note= "CDR1 region"
XX FT misc_feature 100..123
XX FT /*tag= d
XX FT /note= "FR2 region"
XX FT misc_feature 134..141
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XX FT /note= "FR4 region"
XX
XX WO200253595-A1.
XX
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI; 2002-583604/62.
XX P-PSDB; ABG30446.
XX
XX Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
XX variable region of group 2 allergen specific-human IgE Fabs, useful for
XX diagnosing or passive immunotherapy of type I allergy, for environmental
XX allergen detection.
XX
XX Disclosure; Page 32; 45pp; English.
XX
XX This invention relates to the DNA and protein sequences of group 2
XX allergen-specific human IgE Fabs and methods for their use. The proteins
XX of the invention may have anti-allergic activities and may be used as a
XX vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
XX antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
XX 2 allergen-specific fabs of the invention may be useful for environmental
XX allergen detection and for standardisation of allergen extracts. The fabs
XX - or a vaccine against a type I allergy is useful for passive
XX immunotherapy of type I allergy, it is also useful for diagnosing a type
XX I allergy. The allergen-specific fabs of the invention are useful for
XX inter alia, diagnosis, therapy and prevention of type I allergy. They are
XX also useful for identification of group 2 allergen-containing pollen and
```


CC may be used for blocking the binding of grass pollen allergic patients
CC IGE antibodies to Phi p 2. The present sequence represents the DNA
CC encoding the human IgG fab, clone 60 heavy chain protein of the invention
XX
SQ Sequence 342 BP; 70 A; 105 C; 90 G; 77 T; 0 U; 0 Other;

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Query Match          94.4%; Score 322.8; DB 6; Length 342;
Best Local Similarity 96.5%; Pred. No. 3.6e-81;
Matches 330; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACCTGTC 60

QY 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGATCCGCCAGGTCACAGG 120
Db 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTATTGGAGTTGGTCCGCCAGCTCCAGG 120

QY 121 AAGGCCCTGGAGTGGATCGGTACATCTATCACAGTGGCAACCTACAAACCCGTC 180
Db 121 AAGGCCCTGGAGTGGATCGGCAACATCTATCACAGTGGCAACCTACAAACCCGTC 180

QY 181 CTCAGAGTCTGAGTTACCATGTCTAGTAGACACGTCCTAAGAACCCACTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCTGAAATTACCATGTCTAGTAGACACGTCCTAAGAACCCACTTCTCCCTGAGACTG 240

QY 241 AGCTCTGTGACTCGCGGACAGCGCCGTGTATTACTGTGGAGTCAAGTGGGTACACT 300
Db 241 ACCTCTGTGACTCGCGGACAGCGCCGTCTATTACTGTGGCGGTCAAGTGGGTATACT 300

QY 301 TTGGACAACCTGGGCCAGGAAACCTGTCTACCGTCTCCTCA 342
Db 301 TTGGACAACCTGGGCCAGGAAACCTGTCTACCGTCTCCTCA 342
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RESULT 3

ABK89637
ID ABK89637 standard; DNA; 342 BP.

AC ABK89637;

DT 21-OCT-2002 (first entry)

DE DNA encoding human IgE Fab clone 94 heavy chain.

XX Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;
KW timothy grass pollen allergen; passive immunotherapy.

XX Homo sapiens.

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Key Location/Qualifiers
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FT /product= "Fab clone 94 heavy chain"
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FT misc_feature 79..99
FT /tag= c
FT /note= "CDR1 region"
FT misc_feature 100..123
FT /tag= d
FT /note= "FR2 region"
FT misc_feature 134..141
FT /tag= e
FT /note= "FR3 region"
FT misc_feature 142..189
FT /tag= f
FT /note= "CDR2 region"
FT misc_feature 190..285
FT /tag= g
FT /note= "FR3 region"
FT misc_feature 286..309
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FT /tag= h
FT /note= "CDR3 region"
FT misc_feature 310..342
FT /tag= i
FT /note= "FR4 region"
XX
XX WO200253595-A1.
XX
XX 11-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-SE002908.
XX
XX 29-DEC-2000; 2000SE-00004892.
XX
XX (PHAA ) PHARMACIA DIAGNOSTICS AB.
XX
XX Flicker S, Steinberger P, Kraft D, Valenta R;
XX
XX WPI; 2002-583604/62.
XX P-FSDB; ABG30445.
```

Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising variable region of group 2 allergen specific-human IgE Fabs, useful for diagnosing or passive immunotherapy of type I allergy, for environmental allergen detection.

Disclosure; Page 31-32; 45pp; English.

This invention relates to the DNA and protein sequences of group 2 allergen-specific human IgE Fabs and methods for their use. The proteins of the invention may have antiallergic activities and may be used as a vaccine or an inhibitor of binding of grass pollen allergic patient's IgE antibodies to Phi p 2 (a major timothy grass pollen allergen). The group 2 allergen-specific fabs of the invention may be useful for environmental allergen detection and for standardisation of allergen extracts. The fabs - or a vaccine against a type I allergy is useful for passive immunotherapy of type I allergy, it is also useful for diagnosing a type I allergy. The allergen-specific fabs of the invention are useful for inter alia, diagnosis, therapy and prevention of type I allergy. They are also useful for identification of group 2 allergen-containing pollen and may be used for blocking the binding of grass pollen allergic patients IGE antibodies to Phi p 2. The present sequence represents the DNA encoding the human IgG fab, clone 94 heavy chain protein of the invention

SQ Sequence 342 BP; 69 A; 100 C; 98 G; 75 T; 0 U; 0 Other;

Query Match 90.2%; Score 308.4; DB 6; Length 342;
Best Local Similarity 93.9%; Pred. No. 4.1e-77;
Matches 321; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGTC 60

QY 61 TCTGTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGATCCGCCAGGTCACAGG 120
Db 61 TCTGGCGGCTCCATCCGAGTGGTGGTTACTTACTTGGAGTTGGATCCGCCAACACCCAGG 120

QY 121 AAGGCCCTGGAGTGGATCGGGTACATCTATCACAGTGGCAACACCTACAAACCCGTC 180
Db 121 AAGGCCCTGGAGTGGATTTGGGTACATCTATCACAGTGGGAACACCTACTACACCCGTC 180

QY 181 CTCAGAGTCTGAGTTACCATGTCTAGTAGACACGTCCTAAGAACCCACTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCTGAAATTGCCATGTCTGAGTAGACACGTCCTGAGAACAAAGTTCTCCCTGAGGCTG 240

QY 241 AGCTCTGTGACTCGCGGACAGCGCCGTGTATTACTGTGCGAGTCAAGTGGGTACACT 300
Db 241 AACTCTGTGACTCGCGGACAGCGCCGTGTATTACTGTGCGAGTGTAGATGGGTACACT 300

QY 301 TTGGACAACCTGGGCCAGGAAACCTGTCTACCGTCTCCTCA 342
Db 301 TTGGACAACCTGGGCCAGGAAACCTGTCTACCGTCTCCTCA 342
```

```
RESULT 4
ADC99786
ID   ADC99786 standard; DNA; 352 BP.
XX
AC   ADC99786;
XX
DT   01-JAN-2004 (first entry)
XX
DE   Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 15.
XX
KW   anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW   cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW   cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW   lung cancer; human; ds; gene.
XX
OS   Homo sapiens.
XX
PN   WO2003057838-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US041581.
XX
PR   28-DEC-2001; 2001US-0346299P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Gudas J;
XX
DR   WPI; 2003-587113/55.
XX
DR   P-PSDB; ADC99784.
XX
PT   New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT   or condition associated with expression of MUC18 in a patient, e.g.
PT   tumors, cancers, and other malignancies.
XX
PS   Claim 8; SEQ ID NO 15; 78pp; English.
XX
CC   The invention relates to a novel isolated monoclonal antibody comprising
CC   a heavy or light chain amino acid or a heavy or light chain variable
CC   domain where the antibody binds to MUC18. The monoclonal antibody of the
CC   invention demonstrates cytostatic activity and may be useful for treating
CC   a disease or condition associated with the expression of MUC18 on the
CC   cell surface such as tumours, specifically melanoma, oesophageal,
CC   pancreatic or colorectal tumours, carcinomas, particularly cervical
CC   carcinomas and cervical intraepithelial neoplasia and cancers including
CC   colorectal, breast or lung cancer, as well as other malignancies. The
CC   current sequence is that of the anti-human MUC18 monoclonal antibody
CC   heavy chain variable domain DNA of the invention.
XX
SQ   Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match      83.2%; Score 284.6; DB 9; Length 352;
Best Local Similarity 92.0%; Pred. No. 2.1e-70;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY   4 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACTGCTCT 63
DB   16 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACTGCTCT 75

QY   64 GGTGGCTCCATCCGAGTGGTGGTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
DB   76 GGTGGCTCCATCAGCAGTGGTGGTACTACTGGACTTGGATCCGCGAGCACCAGGGAAG 135

QY   124 GGCCTGGAGTGGATCGGGTACATCTATCTACAGTGGCAACACCTTACAAACCCGCTCCCTC 183
DB   136 GGCCTGGAGTGGATCGGGTTCATCTATTACAGTGGGAGCACCTTACTACAAACCCGCTCCCTC 195

QY   184 AAGAGTTCGAGTTACCATGTCAGTACAGTCTTACAGAACCTTCTCCCTGAGGCTGAGC 243
DB   196 AAGAGTTCGAGTTACCATGTCAGTACAGTCTTACAGAACCTTCTCCCTGAGGCTGAGC 255
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QY   244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGTCAAGTGGTACACTTTG 303
DB   256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAG--AGAGGGAGATGCTTT 312

QY   304 GACAACTGGGGCCAGGGAACTGTGTCAACCGTCTCTCTCA 342
DB   313 GACTACTGGGGCCAGGGAACTGTGTCAACCGTCTCTCTCA 351

RESULT 5
ADD05390
ID   ADD05390 standard; DNA; 352 BP.
XX
AC   ADD05390;
XX
DT   01-JAN-2004 (first entry)
XX
DE   Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 15.
XX
KW   monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW   antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003057006-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US041582.
XX
PR   28-DEC-2001; 2001US-0346460P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Gudas J, Bar-Eli M;
XX
DR   WPI; 2003-577496/54.
XX
DR   P-PSDB; ADD05388.
XX
PT   Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT   treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT   associated with melanoma, or increasing survival of an animal having a
PT   metastatic tumor.
XX
PS   Disclosure; SEQ ID NO 15; 87pp; English.
XX
CC   The invention relates to a novel monoclonal antibody used for inhibiting
CC   tumour growth in an animal. The tumour inhibition process comprises
CC   selecting an animal in need of treatment for a tumour, providing a
CC   monoclonal antibody comprising a heavy chain amino acid, where the
CC   antibody consists of any one of 10 fully defined sequences of 117-123
CC   amino acids given in the specification, and where the monoclonal antibody
CC   binds MUC18, and contacting the tumour with the antibody resulting in
CC   inhibited proliferation of the cells. The monoclonal antibody has
CC   cytostatic and can be used in the production of a vaccine. The monoclonal
CC   antibodies against the MUC18 antigen are useful for diagnosing and
CC   treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC   tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC   increasing survival of an animal having a metastatic tumour. This
CC   polynucleotide sequence represents the DNA encoding an anti-MUC18
CC   antibody heavy chain, variable region, protein of the invention.
XX
SQ   Sequence 352 BP; 73 A; 100 C; 103 G; 76 T; 0 U; 0 Other;

Query Match      83.2%; Score 284.6; DB 9; Length 352;
Best Local Similarity 92.0%; Pred. No. 2.1e-70;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY   4 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACTGCTCT 63
DB   16 GAGTCTGCCCGGAGCTGGTGAAGCCTTCACAGACCCCTGCTCCCTCACCTGCACTGCTCT 75
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QY 64 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTACAACACCCCGTCCCTC 183
Db 136 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGGAGCACCTACTACAACCCCGTCCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACACCGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATGTCTAGTAGACACCGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTCGCGGGACACGGCGGTGTATTACTGTGGAGTCAAGTGGGTACTGTTG 303
Db 256 TCTGTGACTCGCGGGACACGGCGGTGTATTACTGTGGAGTCAAGTGGGTACTGTTG 312
QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
Db 313 GACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 351

RESULT 6

AAF29076
ID AAF29076 standard; DNA; 360 BP.

AC AAF29076;

XX DT 03-APR-2001 (first entry)

XX DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 32.

XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
envelope glycoprotein; gp120; diagnosis; ds.

XX OS Homo sapiens.

XX PN WO200100678-A1.

XX PD 04-JAN-2001.

XX PF 23-JUN-2000; 2000WO-US017327.

XX PR 30-JUN-1999; 99US-0141701P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Watkins BA, Reitz MS;

XX DR WPI; 2001-112438/12.

XX DR P-PSDB; AAB62775.

XX PT Novel human monoclonal antibody immunoreactive with human
immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
in biological sample and providing passive immunotherapy to HIV-1
infected mammal.

XX PS Claim 4; Page 45; 81pp; English.

XX CC The present invention provides the protein and coding sequences for the
variable regions of human monoclonal antibodies which are immunoreactive
with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX CC These can be used in diagnosis and therapy of HIV-1 infection

XX SQ Sequence 360 BP; 73 A; 104 C; 107 G; 76 T; 0 U; 0 Other;

Query Match 83.2%; Score 284.4; DB 4; Length 360;

Best Local Similarity 91.5%; Pred. No. 2.5e-70;

Matches 313; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTGTCTCT 63

Db 19 GAGTGGGCCAGGACTGGTGAAGCCTTACAGACCCCTGTCCTCACCTGCACTGTCTCT 78

QY 64 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 79 GGTGGCTCCATCCGACGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 138
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGAGTGGCAACCTACAACACCCCGTCCCTC 183
Db 139 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGGAGCACCTACTACAACCCCGTCCCTC 198
QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACACCGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 199 AAGAGTCGAGTTACCATGTCTAGTAGACACCGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 258
QY 244 TCTGTGACTCGCGGGACACGGCGGTGTATTACTGTGGAGTCAAGTGGGTACTGTTG 300
Db 259 TCTGTGACTCGCGGGACACGGCGGTGTATTACTGTGGAGTCAAGTGGGTACTGTTG 318
QY 301 TTGGACAACCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 342
Db 319 TTGGACCCTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCA 360

RESULT 7

ADC99778
ID ADC99778 standard; DNA; 352 BP.

AC ADC99778;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 7.

XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
lung cancer; human; ds; gene.

XX OS Homo sapiens.

XX PN WO2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX PI WPI; 2003-587113/55.

XX DR P-PSDB; ADC99776.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
or condition associated with expression of MUC18 in a patient, e.g.
tumors, cancers, and other malignancies.

XX PS Claim 8; SEQ ID NO 7; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising
a heavy or light chain amino acid or a heavy or light chain variable
domain where the antibody binds to MUC18. The monoclonal antibody of the
invention demonstrates cytostatic activity and may be useful for treating
a disease or condition associated with the expression of MUC18 on the
cell surface such as tumours, specifically melanoma, oesophageal,
pancreatic or colorectal tumours, carcinomas, particularly cervical
carcinomas and cervical intraepithelial neoplasia and cancers including
colorectal, breast or lung cancer, as well as other malignancies. The
current sequence is that of the anti-human MUC18 monoclonal antibody
heavy chain variable domain DNA of the invention.

XX SQ Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 80.4%; Score 275; DB 9; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.1e-67;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;
QY 4 GAGTTCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTACCTGCACTGTCTCT 63
DB 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTACCTGCACTGTCTCT 75
QY 64 GTGGCTCCATCGCAGTGGTGTATTACTCGAGTTGGATCGCCAGCGTCCAGGGAAG 123
DB 76 GTGGCTCCATCAGCAGTGGTGTATTACTCGAGTTGGATCGCCAGCACCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTTACAAACCCGTCCTCTC 183
DB 136 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGGAGCACCCTACTACACCCGTCCTCTC 195
QY 184 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 312
QY 304 GACAACTGGGGCCAGGGAACCCCTGCTCACCCTGCTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGGAACCCCTGCTCACCCTGCTCTCTCA 351

RESULT 8
ADD05382
ID ADD05382 standard; DNA; 352 BP.
XX
AC ADD05382;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 7.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003057006-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US041582.
XX
PR 28-DEC-2001; 2001US-0346460P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas J, Bar-Eli M;
XX
DR WPI; 2003-577496/54.
DR P-PSDB; ADD05380.
XX

Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumor.

Disclosure; SEQ ID NO 7; 87pp; English.

The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123

CC amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in CC inhibited proliferation of the cells. The monoclonal antibody has CC cytostatic and can be used in the production of a vaccine. The monoclonal CC antibodies against the MUC18 antigen are useful for diagnosing and CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or CC tumour metastasis), inhibiting cell invasion associated with melanoma, or CC increasing survival of an animal having a metastatic tumour. This CC polynucleotide sequence represents the DNA encoding an anti-MUC18 CC antibody heavy chain, variable region, protein of the invention.

XX
SQ Sequence 352 BP; 76 A; 102 C; 103 G; 71 T; 0 U; 0 Other;

Query Match 80.4%; Score 275; DB 9; Length 352;
Best Local Similarity 90.3%; Pred. No. 1.1e-67;
Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTTCGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTACCTGCACTGTCTCT 63
DB 16 GAGTCGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGCTCCCTACCTGCACTGTCTCT 75
QY 64 GTGGCTCCATCGCAGTGGTGTATTACTCGAGTTGGATCGCCAGCGTCCAGGGAAG 123
DB 76 GTGGCTCCATCAGCAGTGGTGTATTACTCGAGTTGGATCGCCAGCACCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTTACAAACCCGTCCTCTC 183
DB 136 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGGAGCACCCTACTACACCCGTCCTCTC 195
QY 184 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCGCGGACACGCGCGGTATTACTGTGCGAGTTCAGATGGGTACACTTTG 312
QY 304 GACAACTGGGGCCAGGGAACCCCTGCTCACCCTGCTCTCTCA 342
DB 313 AAGTACTGGGGCCAGGGAACCCCTGCTCACCCTGCTCTCTCA 351

RESULT 9
AAF29046
ID AAF29046 standard; DNA; 369 BP.
XX
AC AAF29046;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 2.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis; ds.
XX
OS Homo sapiens.
XX
PN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US017327.
XX
PR 30-JUN-1999; 99US-0141701P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
DR P-PSDB; AAB62745.
XX
PT Novel human monoclonal antibody immunoreactive with human

```
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
XX infected mammal.
XX
XX Claim 4; Page 34-35; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection
XX
XX Sequence 369 BP; 75 A; 104 C; 107 G; 83 T; 0 U; 0 Other;
SQ
    Query Match      80.1%; Score 273.8; DB 4; Length 369;
    Best Local Similarity 88.9%; Pred. No. 2.4e-67;
    Matches 312; Conservative 0; Mismatches 27; Indels 12; Gaps 1;
XX
QY 4 GAGTGTGCTCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db |||||
XX 19 GAGTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 78
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db |||||
XX 79 GGTGCTCCATCAGCAGTGGTGGTTACTACTGGAGTGGATCCGCCAGCACCAGGGAAG 138
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCACAACCTCAACAACCCGTCCTC 183
Db |||||
XX 139 GGCCTGGAGTGGATGGGGTACATCTATACAGTGGGAGCACCCTACACAACCCGTCCTC 198
QY 184 AAGAGTGGAGTTACCATGTTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db |||||
XX 199 AAGAGTGGAGTTACCATATCAATAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 258
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGTC-----AGAT 291
Db |||||
XX 259 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGGCGCGGTATTGTGGTGGT 318
QY 292 GGGTACACTTTGGACAACATGGGGCCAGGGAACCCCTGTCACCGTCTCCTCA 342
Db |||||
XX 319 GATTGCTCCTTTGACTACTGGGGCCAGGGAACCCCTGTCACCGTCTCCTCA 369

RESULT 10
ADC99798
XX ID ADC99798 standard; DNA; 358 BP.
XX AC ADC99798;
XX
XX 01-JAN-2004 (first entry)
XX
XX Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 27.
XX
KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
KW lung cancer; human; ds; gene.
XX
XX Homo sapiens.
XX
XX WO2003057838-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041581.
XX
XX 28-DEC-2001; 2001US-0346299P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas J;
XX
XX WPI; 2003-587113/55.
XX
XX P-PSDB; ADC99796.
XX
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XX New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
PT tumors, cancers, and other malignancies.
XX
XX Claim 8; SEQ ID NO 27; 78pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
XX
XX Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;
SQ
    Query Match      78.5%; Score 268.4; DB 9; Length 358;
    Best Local Similarity 88.6%; Pred. No. 8e-66;
    Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
XX
QY 4 GAGTGTGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db |||||
XX 16 GAGTGGGCCCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db |||||
XX 76 GGTGCTCCATCAACAGTGGTGGTTGCTACTGGAGTGGATCCGCCAGCACCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCACAACCTCAACAACCCGTCCTC 183
Db |||||
XX 136 GGCCTGGAGTGGATGGGTACATCTATTCCAGTGGGAGCACCTACTACAACCCGTCCTC 195
QY 184 AAGAGTGGAGTTACCATGTTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db |||||
XX 196 AAGAGTGGAGTTACCTTATCTATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGCGAG---GTCAGATGGGTACACT 300
Db |||||
XX 256 TCTATGACTGCGCGGACACGCGCGTGTATTACTGTGCGAGAGATCGGGAACAGCTGGT 315
QY 301 TTGGACAACCTGGGCGCAGGGAACCCCTGCTACCCGTCCTCTCA 342
Db |||||
XX 316 TTTGACTACTGGGCGCAGGGAACCCCTGCTACCCGTCCTCTCA 357

RESULT 11
ADD05402
XX ID ADD05402 standard; DNA; 358 BP.
XX AC ADD05402;
XX
XX 01-JAN-2004 (first entry)
XX
XX Anti-MUC18 antibody heavy chain variable region DNA, SEQ ID No 27.
XX
KW monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
KW antigen; tumour metastasis; melanoma; metastatic; human; heavy chain;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003057006-A2.
XX
XX 17-JUL-2003.
XX
XX 26-DEC-2002; 2002WO-US041582.
XX
XX 28-DEC-2001; 2001US-0346460P.
XX
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XX (ABGE-) ABGENIX INC.
XX Gudas J, Bar-Eli M;
XX WPI; 2003-577496/54.
XX P-PSDB; ADD05400.
XX Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
PT treating tumors, inhibiting tumor growth, inhibiting cell invasion
PT associated with melanoma, or increasing survival of an animal having a
XX metastatic tumor.
XX Disclosure; SEQ ID NO 27; 87pp; English.
XX The invention relates to a novel monoclonal antibody used for inhibiting
CC tumour growth in an animal. The tumour inhibition process comprises
CC selecting an animal in need of treatment for a tumour, providing a
CC monoclonal antibody comprising a heavy chain amino acid, where the
CC antibody consists of any one of 10 fully defined sequences of 117-123
CC amino acids given in the specification, and where the monoclonal antibody
CC binds MUC18, and contacting the tumour with the antibody resulting in
CC inhibited proliferation of the cells. The monoclonal antibody has
CC cytostatic and can be used in the production of a vaccine. The monoclonal
CC antibodies against the MUC18 antigen are useful for diagnosing and
CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
CC increasing survival of an animal having a metastatic tumour. This
CC polynucleotide sequence represents the DNA encoding an anti-MUC18
CC antibody heavy chain, variable region, protein of the invention.
XX
SQ Sequence 358 BP; 77 A; 103 C; 101 G; 77 T; 0 U; 0 Other;

Query Match 78.5%; Score 268.4; DB 9; Length 358;
Best Local Similarity 88.6%; Pred. No. 8e-66;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;
QY 4 GAGTCGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 63
DB 16 GAGTCGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCT 75
QY 64 GTTGGCTCATCGCGAGTGGTGGTTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
DB 76 GTTGGCTCATCAACAGTGGTGGTTACTTGGAGCTGGATCCGCGAGCACCCAGGGAAG 135
QY 124 GGCTCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 183
DB 136 GGCTCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 195
QY 184 AAGAGTCGAGTTACCAATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCAATGTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGAGACAGCGCGGTGTTACTGTGGAG---GTCAGATGGGTACACT 300
DB 256 TCTATGACTGCGCGAGACAGCGCGGTGTTACTGTGGAGAGATCGGGAACAGCTGGT 315
QY 301 TTGGCAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
DB 316 TTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 357

RESULT 12
AAA46876
ID AAA46876 standard; DNA; 516 BP.
XX
AC AAA46876;
XX
XX 03-OCT-2000 (first entry)
XX
DE DNA encoding the heavy chain of immunoglobulin clone 2.1.3.
XX
KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

KW hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW proliferative disorder; cancer; immunodeficient disorder; ss.
XX Homo sapiens.
XX WO200037504-A2.
XX 29-JUN-2000.
XX 23-DEC-1999; 99WO-US030895.
XX 23-DEC-1998; 98US-0113647E.
XX (PFIZ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG;
PI Corvalan JR;
XX WPI; 2000-442647/38.
XX P-PSDB; AAY93713.
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT -4 containing specified heavy and light chain sequences, useful for
PT treating, e.g. immune disorders.
XX Example 2; Fig 1G; 157pp; English.
XX The present sequence encodes a heavy chain of an antibody of the
CC invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC -4. Antibodies of the invention are composed of a heavy chain variable
CC region, comprising a modified contiguous sequence from a FRI-PR3 sequence
CC encoded by a human VH3-33 family gene. The modifications are contained in
CC CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC used to up-regulate immune system to up-regulate immunodeficient
CC disorders.
XX
SQ Sequence 516 BP; 103 A; 167 C; 142 G; 104 T; 0 U; 0 Other;

Query Match 78.1%; Score 267.2; DB 3; Length 516;
Best Local Similarity 88.6%; Pred. No. 1.9e-65;
Matches 303; Conservative 0; Mismatches 33; Indels 6; Gaps 1;
QY 7 TCTGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCTGGT 66
DB 1 TCGGGCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACCTGTCTCTGGT 60
QY 67 GGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAGGC 126
DB 61 GGCTCCATCAGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 127 CTGGAGTGGATCGGTGTACATCTATCAGTGGCAACCTACAAACCCGCTCCCTCAAG 186
DB 121 CTGGAGTGGATCGGTGTACATCTATCAGTGGCAACCTACAAACCCGCTCCCTCAAG 180
QY 187 AGTCCAGTTACCATGTCAGTAGACAGCTTAGAACCACTTCTCCCTGAGGCTGAGCTCT 246
DB 181 AGTCCAGTTACCATGTCAGTAGACAGCTTAGAACCACTTCTCCCTGAGGCTGAGCTCT 240
QY 247 GTGACTGCGCGGACACCGCCGTGTATTACTGTGCGAGTGCAGTGGG-----TACACT 300
DB 241 GTGACTGCGCGGACACCGCCGTGTATTATTGTGGAGAGATAGTGGGACTACTACGCT 300
QY 301 TTGGCAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
DB 301 ATAGACGTCTGGGGCCAGGGAACCCAGCGGTCAACCGTCTCTCTCA 342

RESULT 13
AAP29066

```

ID AAF29066 standard; DNA; 366 BP.
XX
AC AAF29066;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 22.
XX
XX Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX envelope glycoprotein; gp120; diagnosis; ds.
XX
OS Homo sapiens.
XX
XX WO200100678-A1.
XX
XX 04-JAN-2001.
XX
XX 23-JUN-2000; 2000WO-US017327.
XX
XX 30-JUN-1999; 99US-0141701P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Watkins BA, Reitz MS;
XX
XX WPI; 2001-112438/12.
XX
XX P-PSDB; AAB62765.
XX
XX Novel human monoclonal antibody immunoreactive with human
XX immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX in biological sample and providing passive immunotherapy to HIV-1
XX infected mammal.
XX
XX Claim 4; Page 42; 81pp; English.
XX
XX The present invention provides the protein and coding sequences for the
XX variable regions of human monoclonal antibodies which are immunoreactive
XX with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX These can be used in diagnosis and therapy of HIV-1 infection
XX
XX Sequence 366 BP; 73 A; 107 C; 106 G; 80 T; 0 U; 0 Other;
XX
XX Query Match 77.2%; Score 264; DB 4; Length 366;
XX Best Local Similarity 87.4%; Pred. No. 1.4e-64;
XX Matches 304; Conservative 0; Mismatches 35; Indels 9; Gaps 1;
XX
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 63
DB 19 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 78
QY 64 GGTGGCTCCATCCGACGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
DB 79 GGTGGCTCCATCCGACGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 138
QY 124 GGCTTGAGTGGATCGGGTACATCTATCAGTGGGCAACACCTACACCAACCCGTCCTC 183
DB 139 GGCTTGAGTGGATCGGGTACATCTATCAGTGGGAGCACCTACTACACCCGTCCTC 198
QY 184 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 199 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 258
QY 244 TCTGTGACTGCGGGACAGCGCGGTGTATTACTGTGCGGAGGATGCTACGGGACTCT 294
DB 259 TCTGTGACTGCGGGACAGCGCGGTGTATTACTGTGCGGAGGATGCTACGGGACTCT 318
QY 295 TACACTTTGGACAACTCGGGCCAGGGAAACCTGGTCAACCGTCTCCTCA 342
DB 319 ACTGGACTGTGCTACTGGGGCCGTGGCACCCTGTGCTACTGTCTCTCA 366

ID AAQ38670 standard; cDNA; 357 BP.
XX
XX AAQ38670;
XX
DT 25-MAR-2003 (revised)
XX
DT 06-MAY-1993 (first entry)
XX
DE MAB GAH variable region of heavy chain.
XX
XX Monoclonal antibody; hybridoma; PCR; variable region; constant region;
XX heavy chain; light chain; ss.
XX
XX Synthetic.
XX
XX EP520499-A1.
XX
XX 30-DEC-1992.
XX
XX 26-JUN-1992; 92EP-00110841.
XX
XX 28-JUN-1991; 91JP-00158859.
XX
XX 28-JUN-1991; 91JP-00158860.
XX
XX 28-JUN-1991; 91JP-00158861.
XX
XX (MITU ) MITSUBISHI KASEI CORP.
XX
XX Hosokawa S, Tagawa T, Hirakawa Y, Ito N, Nagaike K;
XX
XX WPI; 1993-001328/01.
XX
XX P-PSDB; AAR30143.
XX
XX Human monoclonal antibody specific for a cancer cell membrane surface
XX antigen - prepd. from a hybridoma obtd. by cell fusion between human
XX lymphocytes derived from cancer patients and mouse myeloma cells.
XX
XX Claim 13; Page 31 + 14-15; 37pp; English.
XX
XX A human MAB specifically binding to a surface antigen of cancer cell
XX membrane comprises variable regions of the heavy and light chains having
XX the amino acid sequences of AAR30143-44 respectively, encoded by DNA
XX sequences AAQ38670 and AAQ33032 respectively. (Updated on 25-MAR-2003 to
XX correct PN field.)
XX
XX Sequence 357 BP; 73 A; 105 C; 102 G; 77 T; 0 U; 0 Other;
XX
XX Query Match 77.1%; Score 263.6; DB 2; Length 357;
XX Best Local Similarity 87.7%; Pred. No. 1.8e-64;
XX Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;
XX
QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 63
DB 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCTGTCCCTCACCTGCACCTGTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCGACGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 135
QY 124 GGCTTGAGTGGATCGGGTACATCTATCAGTGGGCAACACCTACAAACCCGTCCTC 183
DB 136 GGCTTGAGTGGATCGGGTACATCTATCAGTGGGAGCACCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGGGACAGCGCGGTGTATTACTGTGCGGAGGTCAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCGGGACAGCGCGGTGTATTACTGTGCGGAGGTCAGATGGGTACACTTTG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
DB 316 GCTGACTACTGGGGCCAGGGAACAAATGGTCAACCGTCTCCTCA 357

RESULT 14
AAQ38670

```

RESULT 15
ADC99806
ID ADC99806 standard; DNA; 352 BP.
XX AC ADC99806;
XX DT 01-JAN-2004 (first entry)
XX DE Anti-human MUC18 antibody heavy chain variable domain DNA SEQ ID 35.
XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
KW cytotstatic; melanoma; oesophageal; pancreatic; colorectal tumour;
KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX lung cancer; human; ds; gene.
OS Homo sapiens.
XX FN WO2003057838-A2.
XX PD 17-JUL-2003.
XX PF 26-DEC-2002; 2002WO-US041581.
XX PR 28-DEC-2001; 2001US-0346299P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas J;
XX DR WPI; 2003-587113/55.
XX DR P-PSDB; ADC99804.
XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
PT or condition associated with expression of MUC18 in a patient, e.g.
XX tumors, cancers, and other malignancies.
XX Claim 8; SEQ ID NO 35; 78pp; English.
XX The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy or light chain amino acid or a heavy or light chain variable
CC domain where the antibody binds to MUC18. The monoclonal antibody of the
CC invention demonstrates cytostatic activity and may be useful for treating
CC a disease or condition associated with the expression of MUC18 on the
CC cell surface such as tumours, specifically melanoma, oesophageal,
CC pancreatic or colorectal tumours, carcinomas, particularly cervical
CC carcinomas and cervical intraepithelial neoplasia and cancers including
CC colorectal, breast or lung cancer, as well as other malignancies. The
CC current sequence is that of the anti-human MUC18 monoclonal antibody
CC heavy chain variable domain DNA of the invention.
SQ Sequence 352 BP; 77 A; 101 C; 105 G; 69 T; 0 U; 0 Other;

Query Match 76.8%; Score 262.8; DB 9; Length 352;
Best Local Similarity 88.2%; Pred. No. 3e-64;
Matches 298; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 5 AGTCTGCCAGGACTGTGAAGCTTCACAGACCTGTCCTCCCTCACCTGCACTGCTCTG 64
DB |||||
QY 17 AGTCGGGCCAGGACTGTGAAGCTTCAGAGACCTGTCCTCCCTCACCTGCACTGCTCTG 76
DB |||||
QY 65 GTGGCTCCATCCGAGTGGTGGTTTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAGG 124
DB |||||
QY 77 GTGGCTCCATCAGCAGTGGTACTTACCACTGGAGTGGATCCGCCAGCACCCAGGAGGG 136
DB |||||
QY 125 GCCTGGAGTGGATCGGTGACATCTATCAGTGGCAACACCTACACACCCGTCCTCA 184
DB |||||
QY 137 GCCTGGAGTGGATGGATACATCTATCAGTGGAGCACCTACCAACCCGTCCTCA 196
DB |||||
QY 185 AGAGTCGAGTTACCATGTCTAGACAGTCTAAGAACCACTTCTCCCTGAGGTGAGCT 244
DB |||||
QY 197 AGAGTCGAGTTACCATGTCTAGACAGTCTAAGAACCACTTCTCCCTGAGGTGAGCT 256
DB |||||

QY 245 CTGTGACTGCCGCGGACACGCGCCGTGTATTACTGTGCGAGGTACAGATGGGTACACTTTGG 304
DB |||||
QY 257 CTGTGACGGCCGCGGACACGCGCCGTGTATTACTGTGCGAG---AGGGGAGATGGCTACA 313
DB |||||
QY 305 ACAACTGGGGCCAGGGAACCCCTGTGTCACCCGTCTCTCA 342
DB 314 GATACTGGGGCCAGGGAACCCCTGTGTCACCCGTCTCTCA 351
DB |||||

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Job time : 223.818 secs

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 03:58:10 ; Search time 760.173 Seconds
(without alignments)
2207.472 Million cell updates/sec

Title: US-10-027-725A-3

Perfect score: 342
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	342	100.0	342	15	US-10-027-725A-3
2	324.4	94.9	342	15	US-10-027-725A-2
3	310	90.6	342	15	US-10-027-725A-1
4	284.6	83.2	352	15	US-10-330-613-15
5	284.6	83.2	352	15	US-10-330-530-15
6	284.6	83.2	352	17	US-10-660-357-15
7	275.8	80.6	663	10	US-09-972-656-79
8	275	80.4	352	15	US-10-330-613-7
9	275	80.4	352	15	US-10-330-530-7
10	275	80.4	352	17	US-10-660-357-7
11	270.8	79.2	370	16	US-10-309-762-186
12	268.4	78.5	358	15	US-10-330-613-27
13	268.4	78.5	358	15	US-10-330-530-27
14	268.4	78.5	358	17	US-10-660-357-27

15	267.8	78.3	429	16	US-10-309-762-110	Sequence 110, App
16	267.6	78.2	370	16	US-10-309-762-189	Sequence 189, App
17	267	78.1	361	16	US-10-309-762-191	Sequence 191, App
18	265	77.5	370	16	US-10-309-762-185	Sequence 185, App
19	264.2	77.3	367	16	US-10-309-762-195	Sequence 195, App
20	262.8	76.8	352	15	US-10-330-613-35	Sequence 35, Appl
21	262.8	76.8	352	15	US-10-330-530-35	Sequence 35, Appl
22	262.8	76.8	352	17	US-10-660-357-35	Sequence 35, Appl
23	261.6	76.5	376	16	US-10-309-762-184	Sequence 184, App
24	261.6	76.5	376	16	US-10-309-762-197	Sequence 197, App
25	261.6	76.5	376	16	US-10-309-762-199	Sequence 199, App
26	261.2	76.4	370	16	US-10-309-762-200	Sequence 200, App
27	260.6	76.2	352	16	US-10-309-762-203	Sequence 203, App
28	260	76.0	376	16	US-10-309-762-187	Sequence 187, App
29	259.6	75.9	519	16	US-10-309-762-174	Sequence 174, App
30	258.6	75.6	382	16	US-10-309-762-194	Sequence 194, App
31	257.4	75.3	361	16	US-10-309-762-193	Sequence 193, App
32	257	75.1	324	9	US-09-864-761-31244	Sequence 31244, A
33	256.4	75.0	370	16	US-10-309-762-201	Sequence 201, App
34	256.4	75.0	370	16	US-10-309-762-212	Sequence 212, App
35	255.8	74.8	450	15	US-10-390-986-13	Sequence 13, Appl
36	253.8	74.2	381	17	US-10-312-316-66	Sequence 66, Appl
37	253.8	74.2	384	17	US-10-312-316-68	Sequence 68, Appl
38	250.6	73.3	381	17	US-10-312-316-64	Sequence 64, Appl
39	248.8	72.7	378	9	US-09-974-449-5	Sequence 5, Appl
40	248.4	72.6	393	9	US-09-925-299-198	Sequence 198, App
41	248.4	72.6	393	10	US-09-925-299-198	Sequence 198, App
42	245.8	71.9	1543	9	US-09-800-729-74	Sequence 74, Appl
43	243.4	71.2	349	12	US-10-269-711-2	Sequence 2, Appl
44	242.4	70.9	417	9	US-09-905-243-7	Sequence 7, Appl
45	240	70.2	462	17	US-10-693-629-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1

US-10-027-725A-3

; Sequence 3, Application US/10027725A

; Publication No. US20030082659A1

; GENERAL INFORMATION:

; APPLICANT: Flicker, Sabine

; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof

; FILE REFERENCE: 25401-4

; CURRENT APPLICATION NUMBER: US/10/027,725A

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/259,436

; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 342

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-027-725A-3

Query Match 100.0%; Score 342; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.4e-102;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTCGAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTC	60
Db	1	CTCGAGTCTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGCACCTGTC	60
Qy	61	TCTGCTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCTCCAGGG	120
Db	61	TCTGCTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCTCCAGGG	120
Qy	121	AAGGCTTGGAGTGGATCGGGTACATCTATCACAGTGGCAACACCTACCAACACCCGTCC	180
Db	121	AAGGCTTGGAGTGGATCGGGTACATCTATCACAGTGGCAACACCTACCAACACCCGTCC	180
Qy	181	CTCAGAGTCGAGTTACCATCGTAGACACGCTCTAAGACCACTTCTCCCTGAGGGTG	240

Db 181 CTCAGAGTCGAGTTACCATGTACATGTACAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTG 240
QY 241 AGCTCTGTGACGCGCGGACACGCGGTGTTACTGTGCGAGGTACAGTGGTACACT 300
Db 241 AGCTCTGTGACGCGCGGACACGCGGTGTTACTGTGCGAGGTACAGTGGTACACT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342

RESULT 2

US-10-027-725A-2
; Sequence 2, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR APPLICATION NUMBER: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-2

Query Match 94.9%; Score 324.4; DB 15; Length 342;
Best Local Similarity 96.8%; Pred. No. 9.3e-97;
Matches 331; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTC 60
QY 61 TCTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGGCAGGCTCAGGG 120
Db 61 TCTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGGCAGGCTCAGGG 120
QY 121 AAGGCCCTGGAGTGGTACATCTATCAGTGGCAACACCTACAAACCCGCTCC 180
Db 121 AAGGCCCTGGAGTGGTACATCTATCAGTGGCAACACCTACAAACCCGCTCC 180
QY 181 CTCAGAGTCGAGTTACATGTACATGTACAGACCTCTAAGAACCACTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCGAAATACCATGTACATGTACAGACCTCTAAGAACCACTTCTCCCTGAGGCTG 240
QY 241 AGCTCTGTGACTGCGCGGACACGCGGTGTTACTGTGCGAGGTACAGTGGTACACT 300
Db 241 ACCTCTGTGACTGCGCGGACACGCGGTGTTACTGTGCGAGGTACAGTGGTACACT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342

RESULT 3

US-10-027-725A-1
; Sequence 1, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; PRIOR APPLICATION NUMBER: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2000-12-29

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-1

Query Match 90.6%; Score 310; DB 15; Length 342;
Best Local Similarity 94.2%; Pred. No. 5.3e-92;
Matches 322; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTC 60
Db 1 CTCGAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTC 60
QY 61 TCTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGGCAGGCTCAGGG 120
Db 61 TCTGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGGCAGGCTCAGGG 120
QY 121 AAGGCCCTGGAGTGGTACATCTATCAGTGGCAACACCTACAAACCCGCTCC 180
Db 121 AAGGCCCTGGAGTGGTACATCTATCAGTGGCAACACCTACAAACCCGCTCC 180
QY 181 CTCAGAGTCGAGTTACATGTACATGTACAGACCTCTAAGAACCACTTCTCCCTGAGGCTG 240
Db 181 CTCAGAGTCGAAATGCCATGTCCGTACACACCTCTGAGAACCAAGTCTCCCTGAGGCTG 240
QY 241 AGCTCTGTGACTGCGCGGACACGCGGTGTTACTGTGCGAGGTACAGTGGTACACT 300
Db 241 AACTCTGTGACTGCGCGGACACGCGGTGTTACTGTGCGAGGTACAGTGGTACACT 300
QY 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
Db 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342

RESULT 4

US-10-330-613-15
; Sequence 15, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENTX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-15

Query Match 83.2%; Score 284.6; DB 15; Length 352;
Best Local Similarity 92.0%; Pred. No. 1.3e-83;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCTGGGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
QY 64 GGTGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGGCAGGCTCAGGGAG 123
Db 76 GGTGCTCCATCAGCAGTGGTGGTTACTTACTGGAGTTGGATCGGCAGGCTCAGGGAG 135
QY 124 GGCCTGGAGTGGATCGGCTACATCTATCAGAGTGGCAACCTACAAACCCGCTCCCTC 183
Db 136 GGCCTGGAGTGGATGGGTTTCATCTATTACAGTGGGAGCACCCTACTACAAACCCGCTCCCTC 195

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QY 184 AGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCCCGGACACCGCGGTGTTACTGTGCGAGGTTCAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCCCGGACACCGCGGTGTTACTGTGCGAG--AGAGGGAGATGGCTTT 312
QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
DB 313 GACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 351

RESULT 5
US-10-330-530-15
; Sequence 15, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-330-530-15

Query Match 83.2%; Score 284.6; DB 15; Length 352;
Best Local Similarity 92.0%; Pred. No. 1.3e-83;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTTTCACAGACCCCTGCTCCCTCAGCTGTCTCT 63
DB 16 GAGTGGGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGCTCCCTCAGCTGTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCGACGTGGTGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTACAAACCCGTCCTC 183
DB 136 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCCCGGACACCGCGGTGTTACTGTGCGAGGTTCAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCCCGGACACCGCGGTGTTACTGTGCGAG--AGAGGGAGATGGCTTT 312
QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
DB 313 GACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 351

RESULT 6
US-10-660-357-15
; Sequence 15, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry I.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ABGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
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; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-660-357-15

Query Match 83.2%; Score 284.6; DB 17; Length 352;
Best Local Similarity 92.0%; Pred. No. 1.3e-83;
Matches 312; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTTTCACAGACCCCTGCTCCCTCAGCTGTCTCT 63
DB 16 GAGTGGGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGCTCCCTCAGCTGTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCGACGTGGTGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTACAAACCCGTCCTC 183
DB 136 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCACTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCCCGGACACCGCGGTGTTACTGTGCGAGGTTCAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCCCGGACACCGCGGTGTTACTGTGCGAG--AGAGGGAGATGGCTTT 312
QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 342
DB 313 GACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCCTCA 351

RESULT 7
US-09-972-656-79
; Sequence 79, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(663)
; US-09-972-656-79

Query Match 80.6%; Score 275.8; DB 10; Length 663;
Best Local Similarity 89.0%; Pred. No. 1.2e-80;
Matches 298; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCTTTCACAGACCCCTGCTCCCTCAGCTGTCTCT 63
DB 16 GAGTGGGGCCAGGACTGGTGAAGCCTTTCACAGACCCCTGCTCCCTCAGCTGTCTCT 75
QY 64 GGTGCTCCATCCGACGTGGTGTATTACTGTGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
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Db 76 GGTGGCTCCATCAGCAGTGGTGTACTCCTGGAGCTGGATCCGGAGCCACCAGGGAAG 135
 QY 124 GGCTTGGAGTGGATCGGTACATCTATCAGTGGCAACACCTACAGAACCCGTCCTC 183
 Db 136 GGCTTGGAGTGGATCGGTACATCTATCAGTGGCAACCTACAGAACCCGTCCTC 195
 QY 184 AAGAGTCGAGTACCATGTCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
 Db 196 AAGAGTCGAGTACCATGTCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
 QY 244 TCTGTGACTGCCGCGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
 Db 256 TCTGTGACTGCCGCGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTT 315
 QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTC 338
 Db 316 GACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTC 350

RESULT 8

US-10-330-613-7
 ; Sequence 7, Application US/10330613
 ; Publication No. US20030147809A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gudas, Jean
 ; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
 ; FILE REFERENCE: ABGENIX.022A
 ; CURRENT APPLICATION NUMBER: US/10/330,613
 ; CURRENT FILING DATE: 2002-12-26
 ; PRIOR APPLICATION NUMBER: 60/346299
 ; PRIOR FILING DATE: 2001-12-16
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 352
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-10-330-613-7

Query Match 80.4%; Score 275; DB 15; Length 352;
 Best Local Similarity 90.3%; Pred. No. 1.9e-80;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
 Db 16 GAGTCTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
 QY 64 GGTGCTCCATCCGCGACGAGTGGTATTACTGGAGTGGATCCGCGAGGTCAGGGAAG 123
 Db 76 GGTGCTCCATCAGCAGTGGTACTTACCACTGGAGTGGATCCGCGAGGTCAGGGAAG 135
 QY 124 GGCTTGGAGTGGATCGGTACATCTATCAGTGGCAACCTACAGAACCCGTCCTC 183
 Db 136 GGCTTGGAGTGGATCGGTACATCTATCAGTGGCAACCTACAGAACCCGTCCTC 195
 QY 184 AAGAGTCGAGTACCATGTCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
 Db 196 AAGAGTCGAGTACCATGTCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
 QY 244 TCTGTGACTGCCGCGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
 Db 256 TCTGTGACTGCCGCGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTT 312
 QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
 Db 313 AAGTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 351

RESULT 9

US-10-330-530-7
 ; Sequence 7, Application US/10330530
 ; Publication No. US20030152514A1
 ; GENERAL INFORMATION:

; APPLICANT: Gudas, Jean
 ; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
 ; FILE REFERENCE: ABGENIX.031A
 ; CURRENT APPLICATION NUMBER: US/10/330,530
 ; CURRENT FILING DATE: 2002-12-26
 ; PRIOR APPLICATION NUMBER: US 60/346414
 ; PRIOR FILING DATE: 2001-12-18
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 352
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-10-330-530-7

Query Match 80.4%; Score 275; DB 15; Length 352;
 Best Local Similarity 90.3%; Pred. No. 1.9e-80;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
 Db 16 GAGTCTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
 QY 64 GGTGCTCCATCCGCGAGTGGTATTACTGGAGTGGATCCGCGAGGTCAGGGAAG 123
 Db 76 GGTGCTCCATCAGCAGTGGTACTTACCACTGGAGTGGATCCGCGAGGTCAGGGAAG 135
 QY 124 GGCTTGGAGTGGATCGGTACATCTATCAGTGGCAACCTACAGAACCCGTCCTC 183
 Db 136 GGCTTGGAGTGGATCGGTACATCTATCAGTGGCAACCTACAGAACCCGTCCTC 195
 QY 184 AAGAGTCGAGTACCATGTCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
 Db 196 AAGAGTCGAGTACCATGTCTAGTAGACAGTCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
 QY 244 TCTGTGACTGCCGCGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTG 303
 Db 256 TCTGTGACTGCCGCGACACGGCGGTATTACTGTGCGAGTCAGATGGGTACACTTTT 312
 QY 304 GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 342
 Db 313 AAGTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCTCA 351

RESULT 10

US-10-660-357-7
 ; Sequence 7, Application US/10660357
 ; Publication No. US20040115205A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bar-Eli, Menashe
 ; APPLICANT: Green, Larry L.
 ; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
 ; FILE REFERENCE: ABGENIX.030C1
 ; CURRENT APPLICATION NUMBER: US/10/660,357
 ; CURRENT FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 10/330,580
 ; PRIOR FILING DATE: 2002-12-26
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 352
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-10-660-357-7

Query Match 80.4%; Score 275; DB 17; Length 352;
 Best Local Similarity 90.3%; Pred. No. 1.9e-80;

Matches 306; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
 Db 16 GAGTCTGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 75

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Qy 64 GGTGGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATCGGCTACATCTATCAGAGTGGCAACACCTACAAACAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATCGGCTACATCTATCAGAGTGGCAACACCTACAAACAACCCGTCCTC 195
Qy 184 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTCGCGGACAGCGCGGTGTATTACTGTGCGAGTCCAGTGGGTACACTTTG 303
Db 256 TCTGTGACTCGCGGACAGCGCGGTGTATTACTGTGCGAGTCCAGTGGGTACACTTTG 312
Qy 304 GACAACTGGGCGCCAGGGAACCCCTGGTCACCGTCTCCCTCA 342
Db 313 AAGTACTGGGCGCCAGGGAACCCCTGGTCACCGTCTCCCTCA 351

RESULT 11
US-10-309-762-186
; Sequence 186, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-309-762-186

Query Match 79.2%; Score 270.8; DB 16; Length 370;
Best Local Similarity 88.1%; Pred. No. 4.6e-79;
Matches 312; Conservative 0; Mismatches 27; Indels 15; Gaps 1;

Qy 4 GAGTCTGGCCGAGGACTGGTGAAGCTTTCAGAGACCCCTGTCCTCAGCTGCTCTCT 63
Db 16 GAGTCTGGCCGAGGACTGGTGAAGCTTTCAGAGACCCCTGTCCTCAGCTGCTCTCT 75
Qy 64 GGTGGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATCGGCTACATCTATCAGAGTGGCAACACCTACAAACAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATCGGCTACATCTATCAGAGTGGCAACACCTACAAACAACCCGTCCTC 195
Qy 184 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTCGCGGACAGCGCGGTGTATTACTGTGCGAGTCCAGTGGGTACACTTTG 300
Db 256 TCTGTGACTCGCGGACAGCGCGGTGTATTACTGTGCGAGTCCAGTGGGTACACTTTG 315
Qy 301 -----TTGGACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCCTCA 342
Db 316 TCGGGGAGTTACCTTGACTACTTGGGGCCAGGGAACCCCTGGTCACCGTCTCCCTCA 369
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RESULT 12
US-10-330-613-27
; Sequence 27, Application US/10330613
; Publication No. US20030147809A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-613-27

Query Match 78.5%; Score 268.4; DB 15; Length 358;
Best Local Similarity 88.6%; Pred. No. 2.9e-78;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

Qy 4 GAGTCTGGCCGAGGACTGGTGAAGCCTTTCAGAGACCCCTGTCCTCAGCTGCTCTCT 63
Db 16 GAGTCTGGCCGAGGACTGGTGAAGCCTTTCAGAGACCCCTGTCCTCAGCTGCTCTCT 75
Qy 64 GGTGGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCGCCAGCGTCCAGGGAAG 135
Qy 124 GGCTGGAGTGGATCGGCTACATCTATCAGAGTGGCAACACCTACAAACAACCCGTCCTC 183
Db 136 GGCTGGAGTGGATCGGCTACATCTATCAGAGTGGCAACACCTACAAACAACCCGTCCTC 195
Qy 184 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATGTTCAGTAGACAGCTCTAAGAACCACTTCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTCGCGGACAGCGCGGTGTATTACTGTGCGAGTCCAGTGGGTACACTTTG 300
Db 256 TCTGTGACTCGCGGACAGCGCGGTGTATTACTGTGCGAGTCCAGTGGGTACACTTTG 315
Qy 301 TTGGACAACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCCTCA 342
Db 316 TTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCCTCA 357

RESULT 13
US-10-330-530-27
; Sequence 27, Application US/10330530
; Publication No. US20030152514A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
; FILE REFERENCE: ABGENIX.031A
; CURRENT APPLICATION NUMBER: US/10/330,530
; PRIOR FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: US 60/346414
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-330-530-27

Query Match 78.5%; Score 268.4; DB 15; Length 358;
Best Local Similarity 88.6%; Pred. No. 2.9e-78;
```

Matches	303;	Conservative	0;	Mismatches	36;	Indels	3;	Gaps	1;
Qy	4	GAGTCTGGCCGAGGACTGGTGAAGCCCTTCACAGACCCCTGTCCCTCACTGCACTGTCTCT	63						
Db	16	GAGTCGGGGCCGAGGACTGGTGAAGCCCTTCACAGACCCCTGTCCCTCACTGCACTGTCTCT	75						
Qy	64	GTGGGCTCCATTCGCGAGTGGTGGTATTACTGGAGTTGGATCGGCCAGCGTCCAGGGAAG	123						
Db	76	GTGGGCTCCATCAACAGTGGTGGTTGCTACTGGAGCTGGATCGGCCAGCACCCAGGGAAG	135						
Qy	124	GGCCTGAGTGGATCGGGTACATCTATCAAGTGGGCAACACTTACAACAACCGTCCCTC	183						
Db	136	GGCCTGAGTGGATTTGGGTACATCTATTCCAGTGGGAGCACTACTACAACCGCTCCCTC	195						
Qy	184	AAGAGTCGAGTTACCATGTTCAGTAGACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC	243						
Db	196	AAGAGTCGAAATACCTTATCAGTAGACAGCTCTAAGAACCAAGTTCTCCCTGAAGCTGAAC	255						
Qy	244	TCTGTGACTGCCGGGACAGCGCCGTGTATTACTGTGCGAG--GTCAAGATGGGTACACT	300						
Db	256	TCTATGACTGCCGGGACAGCGCCGTGTATTACTGTGCGAGAGATCGGHAACAGCTGGT	315						
Qy	301	TTTGACAACCTGGGGCCAGGGAACCTCTGGTCAACCGTCTCTCTCA	342						
Db	316	TTTGACTPACTGGGGCCAGGGAACCTCTGGTCAACCGTCTCTCTCA	357						

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RESULT 14
US-10-660-357-27
; Sequence 27, Application US/10660357
; Publication No. US20040115205A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Eli, Menashe
; APPLICANT: Green, Larry L.
; TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
; TITLE OF INVENTION: ANTIGEN
; FILE REFERENCE: ARGENIX.030C1
; CURRENT APPLICATION NUMBER: US/10/660,357
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 10/330,580
; PRIOR FILING DATE: 2002-12-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-660-357-27

Query Match      78.5%; Score 268.4; DB 17; Length 358;
Best Local Similarity 88.6%; Pred. No. 2.9e-78;
Matches 303; Conservative 0; Mismatches 36; Indels 3; Gaps 1

QY 4 GAGTCTGGCCCGCAGACTGGTGAAGCCCTTCACAGACCCCTGTCCCTCACTGCACTGTCTCT 63
Db 16 GAGTCGGGGCCGAGACTGGTGAAGCCCTTCACAGACCCCTGTCCCTCACTGCACTGTCTCT 75
QY 64 GGTGGCTCCATCCGACGTGGTGGTATTACTTGGAGTTGGATCCGGCAGCGTCCAGGGAG 123
Db 76 GGTGGCTCCATCAACAGTGGTGGTGTCTACTTGGAGCTGGATCCGCCAGCACCCAGGGAG 135
QY 124 GGCTTGGAGTGGATCGGGTACATCTATCAGAGTGGAAACACTTACAACACCGTCCCTC 183
Db 136 GGCTTGGAGTGGATGGGTACATCTATTCAGTGGGACACTACTACAACCGTCCCTC 195
QY 184 AAGAGTCGAGTTTACCATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAATTACCTTATCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGCTGAC 255
QY 244 TCTGTGACTGCCGGCGGACACGGCCGTGTAATTACTGTGGAG---GTCAGATGGGTPACACT 300
Db 256 TCTATGACTGCCGGCGGACACGGCCGTGTAATTACTGTGCGAGAGATCGGGAAACAGCTGCT 315

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Qy	301	TTGACAACTGGGGCCAGGGAACCTTGGTCACCGTCTCCTCA	342
Db	316	TTTGACTACTGGGGCCAGGGAACCTTGGTCACCGTCTCCTCA	357
RESULT 15			
US-10-309-762-110			
; Sequence 110, Application US/10309762			
; Publication No. US20040018198A1			
; GENERAL INFORMATION:			
; APPLICANT: Gudas, Jean			
; APPLICANT: Foltz, Ian			
; APPLICANT: Handa, Masahisa			
; APPLICANT: Gallo, Michael			
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX			
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN			
; FILE REFERENCE: ABGENIX.027A			
; CURRENT APPLICATION NUMBER: US/10/309,762			
; CURRENT FILING DATE: 2002-12-02			
; PRIOR APPLICATION NUMBER: 60/337275			
; PRIOR FILING DATE: 2001-12-03			
; NUMBER OF SEQ ID NOS: 246			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 110			
; LENGTH: 429			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-309-762-110			
Query Match 78.3%; Score 267.8; DB 16; Length 429;			
Best Local Similarity 87.4%; Pred. No. 4.7e-78;			
Matches 312; Conservative 0; Mismatches 27; Indels 18; Gaps 1;			
Qy	4	GAGTCTGGCCAGGACTGGTGAAGCCCTTACAGACCCCTGTCCCTCACCTGCACCTGTCTCT	63
Db	73	GAGTCGGGCCAGGACTGGTGAAGCCCTTACAGACCCCTGTCCCTCACCTGCACCTGTCTCT	132
Qy	64	GGTGGCTCCATNCCGACGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG	123
Db	133	GGTGGCTCCATNCCGACGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCACCAGGGAAG	192
Qy	124	GGCCTGGAGTGGATCGGGTACATCTATCACAGTGGGCAACACCTTACAAACACCCGTCCTC	183
Db	193	GGCCTGGAGTGGATCGGGTACATCTATTAAGTGGGAGACCTTACTAAACCCGTCCTC	252
Qy	184	AAGAGTCGAGTTACCATGTTCAGTAGACAACCTCTAAGAACCACTTCTCCCTGAGCGTCGAGC	243
Db	253	AAGAGTCGAGTTACCATATCAGTAGACAACCTCTAAGAACCACTTCTCCCTGAGCGTCGAGC	312
Qy	244	TCGTGACTGCCCGGACACGGCCGTGTATTACTGTGCGAG-----G	285
Db	313	TCGTGACTGCCCGGACACGGCCGTGTATTACTGTGCGAGAGAGAAATTACGATATTTTG	372
Qy	286	TCAGATGGGTACACTTTTGGACAACTGGGGCCAGGGAACCTCTGGTCACCGTCTCCTCA	342
Db	373	ACTGGTTTCAACTGTGTTTCGACCCCTGGGGCCAGGGAACCTCTGGTCACCGTCTCCTCA	429

Search completed: August 13, 2004, 19:18:22
Job time : 761.173 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:21:37 ; Search time 48.3636 Seconds
(without alignments)
3924.296 Million cell updates/sec

Title: US-10-027-725A-3

Perfect score: 342

Sequence: 1 ctgagctctggccaggact.....ccctggtcaccgtctctca 342

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/ina/5A COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	267.2	78.1	516	4	US-08-472-087-33
2	263.6	77.1	357	1	US-08-360-125-3
3	263.6	77.1	357	2	US-08-450-578-3
4	263.6	77.1	357	2	US-08-017-628-3
5	263.6	77.1	357	2	US-08-014-880-3
6	263.6	77.1	357	4	US-08-450-363-3
7	257	75.1	631	3	US-08-545-809A-31
8	255.8	74.8	450	4	US-08-582-337-13
9	251.8	73.6	1567	3	US-09-049-672A-17
10	245.8	71.9	1543	4	US-09-800-729-74
11	241.8	70.7	366	1	US-08-360-125-9
12	241.8	70.7	366	2	US-08-450-578-9
13	241.8	70.7	366	2	US-08-017-628-9
14	241.8	70.7	366	2	US-08-014-880-9
15	241.8	70.7	366	4	US-08-450-363-9
16	237.8	69.5	1212	3	US-08-545-809A-61
17	233	68.1	800	3	US-08-545-809A-39
18	226.2	66.1	840	3	US-08-260-527-4
19	224.8	65.7	403	3	US-09-042-353-357
20	224.8	65.7	403	4	US-08-758-417A-205
21	220.8	64.6	288	3	US-08-851-362D-7
22	218.6	63.9	732	4	US-08-039-785-56
23	217.8	63.7	357	2	US-08-652-816A-20
24	216.8	63.4	524	3	US-09-042-353-419
25	216.8	63.4	524	4	US-08-758-417A-219
26	216.8	63.4	4926	3	US-09-042-353-418
27	216.8	63.4	4926	4	US-08-758-417A-268

28	216.2	63.2	291	3	US-08-851-362D-11	Sequence 11, Appl
29	215.8	63.1	622	3	US-08-545-809A-59	Sequence 59, Appl
30	215.6	63.0	750	4	US-10-039-785-62	Sequence 62, Appl
31	215.4	63.0	624	3	US-08-545-809A-28	Sequence 28, Appl
32	214.2	62.6	404	4	US-09-042-353-355	Sequence 355, App
33	214.2	62.6	404	4	US-08-758-417A-203	Sequence 203, App
34	212.8	62.2	294	3	US-08-851-362D-3	Sequence 3, Appli
35	212.6	62.2	650	3	US-08-545-809A-4	Sequence 4, Appli
36	211.4	61.8	402	1	US-08-259-372A-5	Sequence 5, Appli
37	211.4	61.8	402	1	US-08-468-671-5	Sequence 5, Appli
38	211	61.7	800	3	US-08-545-809A-55	Sequence 55, Appl
39	210.6	61.6	354	2	US-08-652-816A-23	Sequence 23, Appl
40	209.2	61.2	381	2	US-08-477-553A-45	Sequence 45, Appl
41	208.8	61.1	291	3	US-08-851-362D-9	Sequence 9, Appli
42	208.6	61.0	369	4	US-08-793-450-3	Sequence 3, Appli
43	208.6	61.0	1418	4	US-08-793-450-7	Sequence 7, Appli
44	208.2	60.9	291	3	US-08-851-362D-5	Sequence 5, Appli
45	207.8	60.8	372	2	US-08-477-553A-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1

US-09-472-087-33

; Sequence 33, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, EILLEN E.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GLIMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: ABX-PP1

; CURRENT APPLICATION NUMBER: US/09/472,087

; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/113,647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 33

; LENGTH: 516

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-472-087-33

Query Match 78.1%; Score 267.2; DB 4; Length 516;
Best Local Similarity 88.6%; Pred. No. 5.8e-76;
Matches 303; Conservative 0; Mismatches 33; Indels 6; Gaps 1;

Qy	7	TCTGCCCCAGACTGGTGAAGCCCTTCACAGACCCCTGTCCTCTCAGTGCAGTCTCTCTGGT	66
Db	1	TCGSGCCAGGACTGGTGAAGCCCTTCACAGATCTGTCTCTCTCAGTGCAGTCTCTCTGGT	60
Qy	67	GGCTCCATTCGCGAGTGGTGTATATCTGGAGTTGGATTCGCGCCAGCGTCCAGGGAAGGC	126
Db	61	GGCTCCATCAGCAGTGGTGGTCTACTTGGAGTGGATTCGCGCCAGCAGCCAGGGAAGGC	120
Qy	127	CTGGAGTGGATCGGGTACATCTATCAGAGTGGGGAACACCTTACACACCCGTCCTCAAG	186
Db	121	CTGGAGTGGATCGGGTACATCTATCAGAGTGGGGAACACCTTACACACCCGTCCTCAAG	180
Qy	187	AGTCAGTTACCATGTCTAGTAGACACCTCTAAGAACACCTTCTCCCTGAGGCTGAGTCT	246
Db	181	AGTCAGTTACCATGTCTAGTAGACACCTCTAAGAACACCTTCTCCCTGAGGCTGAGTCT	240
Qy	247	GTGACTCCGCGGACACGGCGGTGTATCTAGTTCGAGGTCAGATGGG-----TACACT	300
Db	241	GTGACTCCGCGGACACGGCGGTGTATCTAGTTCGAGGTCAGATGGG-----TACACT	300

QY 301 TTGGACAACCTGGGGCAGGACCCCTGGTCAACCGTCTCTCA 342
DB 301 ATAGAGCTCTGGGGCCAGGACCAACGGTCAACCGTCTCTCA 342

RESULT 2

US-08-360-125-3
; Sequence 3, Application US/08360125
; Patent No. 5767246

GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA
APPLICANT: Yoshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246ihiko ITO
APPLICANT: Kazuhiro NAGAIKE

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Cell Membrane

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESS: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,125

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/905,534

FILING DATE: June 29, 1992

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 357 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM:

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE: Hybridoma producing human

CELL TYPE: antibody GAH

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-360-125-3

Query Match 77.1%; Score 263.6; DB 1; Length 357;
Best Local Similarity 87.7%; Pred. No. 7e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTCTGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGACCTGCTCT 63
DB 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACCTGACCTGCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCAGCAGTTGGTTTCTACTGGAACCTGGATCCGCCAGCAGCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGGTATCATCTATCACAGTGGAACACTACAAACCCGTCCTC 183
DB 136 GGCCTGGAGTGGATTTGGGTACATCTATTACAGTGGGAGCAGCTACTACAAACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATGTCTAGTACACACGCTTAAGAACCTCTCTCCCTGAGGCTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCTAGTACACACGCTTAAGAACCTCTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGGGGACACGCGCGTGTATTACTGTGCGAGGTGAGATGGGTACACTTTG 303
DB 256 TCTGTGACTGCGGGGACACGCGCGTGTATTACTGTGCGAGGTCTACCCGACTACGGGGG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 342
DB 316 GCTGACTACTGGGGCCAGGGAACAATGGTCAACCGTCTCTCA 357

RESULT 3

US-08-450-578-3
; Sequence 3, Application US/08450578
; Patent No. 5837845

GENERAL INFORMATION:

APPLICANT: Saiko HOSOKAWA

APPLICANT: Yoshiaki TAGAWA

APPLICANT: Yoko HIRAKAWA

APPLICANT: No. 5837845ihiko ITO

APPLICANT: Kazuhiro NAGAIKE

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Cell Membrane

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESS: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

[illegible]

Db 256 TCTCTGACTGCGCGACACGCGCGTGTATTACTGTGCGAGGTCTACCGGACTACGGGG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACATGGTCAACCGTCTCTTCA 357

RESULT 5

US-09-014-880-3
; Sequence 3, Application US/09014880
; Patent No. 5990297
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA et al.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,880
; FILING DATE: January 28, 1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/450,578
; FILING DATE: May 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; CELL TYPE: Hybridoma producing human
; CELL TYPE: antibody GAH

US-09-014-880-3
Query Match 77.1%; Score 263.6; DB 2; Length 357;
Best Local Similarity 87.7%; Pred. No. 7e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

QY 4 GAGTGTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCTCTCT 63
Db 16 GAGTGTGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGCTCTCT 75
QY 64 GGTGGCTCCATCCGAGTGGTGGTATTACTGGAGTGGATCCGCGACGCTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCGAGTGGTGGTATTACTGGAGTGGATCCGCGACGCTCCAGGGAAG 135

QY 124 GSCCTGGAGTGGGTACATCTATCAGTGGCAACACCTACAAACCGTCCCTC 183
Db 136 GGCCTGGAGTGGGTACATCTATCAGTGGGAGCACCTACTACAAACCGTCCCTC 195
QY 184 AAGAGTCGAGTTACCATGTACGACACGTCTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATGTACGACACGTCTAAGAGCCAGTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCGCGGACACGCGCGGTGTATTACTGTGCGAGGTGAGATGGGTACACTTTG 303
Db 256 TCTCTGACTGCGCGGACACGCGCGGTGTATTACTGTGCGAGGTCTACCGGACTACGGGG 315
QY 304 ---GACAACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGGAACATGGTCAACCGTCTCTTCA 357

RESULT 6

US-08-450-363-3
; Sequence 3, Application US/08450363
; Patent No. 6436434
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 6436434ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,363
; FILING DATE: May 25, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992

ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: Hybridoma producing human
CELL TYPE: antibody GAH
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-3

Query Match 77.1%; Score 263.6; DB 4; Length 357;

Best Local Similarity 87.7%; Pred. No. 7e-75;
Matches 300; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

Qy 4 GAGTCTGCCGACGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 63
Db 16 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 75
Qy 64 GGTGGCTCCATCCGACGAGTGGTGTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCAGCAGTGTGGTGTCTACTGGAACTGGATCCGCGAGCACCAGGGAAG 135
Qy 124 GGCCTGGAGTGGGTGATCATCTATCAGTGGCAACACCTACACAAACCCGTCCTC 183
Db 136 GGCCTGGAGTGGGTGATCATCTATCAGTGGGAGCCTACTACAAACCCGTCCTC 195
Qy 184 AAGAGTCGAGTTACCATCTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTACCATCTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGTCCAGATGGGTACACTTTG 303
Db 256 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAGTCTACCCGACTACGGGGG 315
Qy 304 ---GACAACTGGGGCCAGGAAACCCCTGGTCACCGTCTCTCA 342
Db 316 GCTGACTACTGGGGCCAGGAAACAAATGGTACCGTCTCTTCA 357

RESULT 7

US-08-545-809A-31
Sequence 31, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
US-08-545-809A-31

Query Match 75.1%; Score 257; DB 3; Length 631;
Best Local Similarity 94.7%; Pred. No. 1.2e-72;
Matches 266; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 4 GAGTCTGCCGACGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 63
Db 305 GAGTGGGGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCT 364
Qy 64 GGTGGCTCCATCCGACGAGTGGTGTATTACTGGAGTTGGATCCGCGAGCGTCCAGGGAAG 123
Db 365 GGTGGCTCCATCAGCAGTGGTGTATTACTGGAGTGGATCCGCGAGCACCAGGGAAG 424
Qy 124 GGCCTGGAGTGGGTGATCATCTATCAGTGGCAACACCTACAAACCCGTCCTC 183
Db 425 GGCCTGGAGTGGGTGATCATCTATCAGTGGGAGCCTACTACAAACCCGTCCTC 484
Qy 184 AAGAGTCGAGTTACCATCTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 485 AAGAGTCGAGTTACCATCTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 544
Qy 244 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAG 284
Db 545 TCTGTGACTGCGCGGACACGCGCGTGTATTACTGTGGAG 585

RESULT 8

US-08-582-337-13
Sequence 13, Application US/09582337
Patent No. 6562618
GENERAL INFORMATION:
APPLICANT: Japan Tobacco, Inc.
TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor

;; TITLE OF INVENTION: and Medicinal Uses Thereof
;; FILE REFERENCE: J1-009PCT
;; CURRENT APPLICATION NUMBER: US/09/582,337
;; PRIOR FILING DATE: 2000-06-23
;; PRIOR APPLICATION NUMBER: JP P1997-367699
;; PRIOR FILING DATE: 1997-12-25
;; PRIOR APPLICATION NUMBER: JP P1998-356183
;; PRIOR FILING DATE: 1998-12-15
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 450
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(450)
;; NAME/KEY: sig_peptide
;; LOCATION: (1)..(58)
;; NAME/KEY: V_region
;; LOCATION: (59)..(353)
US-09-582-337-13

Query Match 74.8%; Score 255.8; DB 4; Length 450;
Best Local Similarity 87.1%; Pred. No. 2.4e-72;
Matches 311; Conservative 0; Mismatches 27; Indels 19; Gaps 2;
QY 4 GAGTCGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCTCT 63
Db |||||
74 GAGTCGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCTCT 132
QY 64 GGTGGCTCCATCCGACAGTGGTGGTTATTACTGGATTGGATCCGACGGTCCAGGGAAG 123
Db |||||
133 GGTGGCTCCATCCGACAGTGGTGGTTATTACTGGATTGGATCCGACGGTCCAGGGAAG 192
QY 124 GGCCTGGAGTGGATCGGTGTACATCTATCACAGTGGCAACCTTACAAACCCGTCCTC 183
Db |||||
193 GGCCTGGAGTGGATCGGTGTACATCTATCACAGTGGCAACCTTACAAACCCGTCCTC 252
QY 184 AAGAGTCGAGTTACATGTCAGTAGACACGCTTAAGAACCACTTCCCTGAGGCTGAGC 243
Db |||||
253 AAGAGTCGAGTTACATGTCAGTAGACACGCTTAAGAACCACTTCCCTGAGGCTGAGC 312
QY 244 TCTGTGACTCGCGGACACGGCGGTGTATTACTGTGGAGGT----- 286
Db |||||
313 TCTGTGACTCGCGGACACGGCGGTGTATTACTGTGGAGGTATTACTATGATGGT 372
QY 287 -CAGATGGGTACACTTTGGACAACTGGGCGCAGGGAACCTTGGTCAACCGTCTCCTCA 342
Db |||||
373 GGTATTACGACTACTTGTGACTACTTGGGCGCAGGGAACCTTGGTCAACCGTCTCCTCA 429

RESULT 9
US-09-049-672A-17
; Sequence 17, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guesler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/049,672A
;; FILING DATE: HERewith
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Cerrone, Michael C
;; REGISTRATION NUMBER: 39,132
;; REFERENCE/DOCKET NUMBER: PF-0497 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-855-0555
;; TELEFAX: 650-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1567 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: PANTUT01
;; CLONE: 1513264
US-09-049-672A-17
Query Match 73.6%; Score 251.8; DB 3; Length 1567;
Best Local Similarity 84.6%; Pred. No. 7.9e-71;
Matches 302; Conservative 0; Mismatches 37; Indels 18; Gaps 1;
QY 4 GAGTCGCGCCAGGACTGGTGAAGCCTTCACAGACCCCTGTCCTCAGCTGCTCTCT 63
Db |||||
150 GAGTCGCGCCAGGACTGGTGAAGCCTTCGAGACCCCTGTCCTCAGCTGCTCTCT 209
QY 64 GGTGGCTCCATCCGACAGTGGTGGTTATTACTGGAGTTGGATCCGCGACGGTCCAGGGAAG 123
Db |||||
210 GGTGGCTCCATCCGACAGTGGTGGTTATTACTGGAGTTGGATCCGCGACGGTCCAGGGAAG 269
QY 124 GGCCTGGAGTGGATCGGTGTACATCTATCACAGTGGCAACCTTACAAACCCGTCCTC 183
Db |||||
270 GGCCTGGAGTGGATCGGTGTACATCTATCACAGTGGGAGCACCTTCTACAAACCCGTCCTC 329
QY 184 AAGAGTCGAGTTACATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db |||||
330 AAGAGTCGAGTTACATGTCAGTAGACACGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 389
QY 244 TCTGTGACTCGCGGACACGGCGGTGTATTACTGTGGAGGTGAGT----- 292
Db |||||
390 TCTGTGACTCGCGGACACGGCGGTGTATTACTGTGGAGGTGAGT----- 449
QY 293 -----GGTACACTTTGGACAACTGGGCGCAGGGAACCTTGGTCAACCGTCTCCTCA 342
Db |||||
450 GGGGGGAACTACGGTATGGAGCTGTGGGCGCAGGGAACCTTGGTCAACCGTCTCCTCA 506

RESULT 10
US-09-800-729-74
; Sequence 74, Application US/09800729
; Patent No. 6605592
; FILE REFERENCE: PZ044P1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22

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; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 1543
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-800-729-74

Query Match      71.9%; Score 245.8; DB 4; Length 1543;
Best Local Similarity 83.1%; Pred. No. 6.5e-69;
Matches 280; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 4 GAGTCTGCCCGCAGGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT 63
Db 90 GAGTCTGCCCGCAGGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT 149

QY 64 GGTGGCTCCATCCCGCAGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 150 GGTGGCTCCATCCCGCAGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 209

QY 124 GGCTCGAGTGGATCGGGTATCATCTATCACAGTGGCAACCTACAAACCCCGTCCCTC 183
Db 210 GGCTCGAGTGGATGGGTGATCTCTTACATCGGGTCCCTTACTACATCCGTCCTC 269

QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACACGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 270 AAGAGTCGAGTTACCATGTCTAGTAGACACGCTTCTCAGAACCACTTCTCCCTGAGGCTGAGC 329

QY 244 TCTGTGACTCGCGGACACGGCCGTGTATTACTGTGGAGTGCAGTGGTACACTTTG 303
Db 330 TCTGTGACTCGCGGACACGGCCGTGTATTACTGTGGAGTGCAGTGGTACACTTTG 389

QY 304 GACAACTGGGCGCAGGGAACCTGGTCAACCTGCTCCT 340
Db 390 GACGGGTACCGTGGATACCGAGGCTTGTACTACT 426

RESULT 11
US-08-360-125-9
; Sequence 9, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Yoshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL LINE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-9

Query Match      70.7%; Score 241.8; DB 1; Length 366;
Best Local Similarity 83.2%; Pred. No. 6.7e-68;
Matches 292; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

QY 4 GAGTCTGGCCCGCAGGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCTGGCCCGCAGGACTGGTGAAGCCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCT 75

QY 64 GGTGGCTCCATCCCGCAGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCCGCAGTGGTGGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 135

QY 124 GGCCTGGAGTGGATCGGGTATCATCTATCACAGTGGCAACCTACAAACCCCGTCCCTC 183
Db 136 GGCCTGGAGTGGATCGGGTATCATCTATTAGTGGAGCACTACTACAAACCCCGTCCCTC 195

QY 184 AAGAGTCGAGTTACCATGTCTAGTAGACACGCTTAAAGAACCACTTCTCCCTGAGGCTGAGC 243
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Db 196 AAGAGTCGAGTACCATATCCGTAGACACGTCCAGAACGAGTTCTCCCTGAGCTGAGC 255
QY 244 TCTGTGACTGCCCGGACACGGCGGTGTATTACTGTGCGA-----GGTCAGAT 291
Db 256 TCTGTGACCGCGACACACGGGTGTATTACTGTGCGAGGGGGAGCTACGGGGGCTAC 315
QY 292 GGTACACTTTGGACAACCTGGGCGCAGGGAACCCCTGGTCACCGTCTCCCTCA 342
Db 316 TACTACGGTATGGACGCTCTGGGCGCAAGGAGACCAACCGTCACCGTCTCTCTCA 366

RESULT 12

US-08-450-578-9
; Sequence 9, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5837845hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,578
FILING DATE: May 25, 1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:

STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1

; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-9

Query Match 70.7%; Score 241.8; DB 2; Length 366;
Best Local Similarity 83.2%; Pred. No. 6.7e-68;
Matches 292; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

QY 4 GAGTCTGCCCGGAGGACTGTGAAGCCTTTCACAGACCCCTGTCCCTCACCTGCACTGTCTCT 63
Db 16 GAGTCGGGCGCCAGGACTGTGAAGCCTTTCGGAGACCCCTGTCCCTCACCTGCACTGTCTCT 75
QY 64 GGTGGCTCCATCCGCGAGTGGTGGTTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 76 GGTGGCTCCATCCAGCAGTAGTAGTTACTTGGGGCTGGATCCGCCAGCGTCCAGGGAAG 135
QY 124 GGCCTGGAGTGGATCGGOTACATCTATCACAGTGCGAACACACTACAAACCCGTCCTC 183
Db 136 GGGCTGGAGTGGATTGGGAGTATCTATTATAGTGGGAGCACCCTACTACACCCGTCCTC 195
QY 184 AAGAGTCGAGTTACCATCTCAGTACACAGCTTAAGAACCACTTCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTACCATATCCGTAGACACACGTCCTCAAGAACCCAGTTCTCCCTGAGGCTGAGC 255
QY 244 TCTGTGACTGCCGGGACACGCGCGGTGTATTACTGTGCGA-----GGTCAGAT 291
Db 256 TCTGTGACCGCGCGCAGACACGCGTGTATTACTGTGCGAGGGGAGCTACGGGGGCTAC 315
QY 292 GGTACACTTTGGACAACCTGGGCGCAGGGAACCCCTGGTCACCGTCTCTCTCA 342
Db 316 TACTACGGTATGGACGCTCTGGGCGCAGGAGCAGGAGTCCAGGTCACCGTCTCTCTCA 366

RESULT 13

US-09-017-528-9
; Sequence 9, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287hiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125

FILED DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
CELL TYPE: Hybridoma producing human antibody 1-3-1
US-09-014-880-9

Query Match 70.7%; Score 241.8; DB 2; Length 366;
Best Local Similarity 83.2%; Pred. No. 6.7e-68;
Matches 292; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

QY 4 GAGTCTGGCCAGGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGACCTGTCTCT 63
DB 16 GAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTCACTGACCTGTCTCT 75

QY 64 GGTGGCTCCATCCGAGTGGTGGTATTACTGAGTTGGATCCGACCGGTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCGAGTGGTGGTATTACTGAGTTGGATCCGACCGGTCCAGGGAAG 135

QY 124 GGCTGGAGTGGATCGGTGATCTATACAGTGGCAACACCTACAGACCCCTGTCCTCA 183
DB 136 GGCTGGAGTGGATCGGTGATCTATACAGTGGCAACACCTACAGACCCCTGTCCTCA 195

QY 184 AAGAGTCGAGTTACCATGTCCAGTAGACAGTCTTAAGAACCCATTCTCCCTGAGGTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCCAGTAGACAGTCTTAAGAACCCATTCTCCCTGAGGTGAGC 255

QY 244 TCTGTGACTCCCGGACAGCGCGTGTATTACTGTGCGA-----GGTCAGAT 291
DB 256 TCTGTGACTCCCGGACAGCGCGTGTATTACTGTGCGA-----GGTCAGAT 315

QY 292 GGTGACATTTGGACAACCTGGGCGCAGGGAACCTGTCACTGTCCTCA 342
DB 316 TACTACGGTATGACGCTCTGGGCGCAGGGAACCTGTCACTGTCCTCA 366

RESULT 15
US-08-450-363-9
Sequence 9, Application US/08450363
Patent No. 6436434
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 6436434hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
FILED DATE: December 20, 1994
PRIORITY DATE: December 20, 1994
PRIORITY APPLICATION NUMBER: 07/905,534

EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 9
LENGTH: 366
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
US-09-017-628-9

Query Match 70.7%; Score 241.8; DB 2; Length 366;
Best Local Similarity 83.2%; Pred. No. 6.7e-68;
Matches 292; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

QY 4 GAGTCTGGCCAGGAGTGGTGAAGCCTTCACAGACCCCTGTCCTCACTGACCTGTCTCT 63
DB 16 GAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCCCTGTCCTCACTGACCTGTCTCT 75

QY 64 GGTGGCTCCATCCGAGTGGTGGTATTACTGAGTTGGATCCGACCGGTCCAGGGAAG 123
DB 76 GGTGGCTCCATCCGAGTGGTGGTATTACTGAGTTGGATCCGACCGGTCCAGGGAAG 135

QY 124 GGCTGGAGTGGATCGGTGATCTATACAGTGGCAACACCTACAGACCCCTGTCCTCA 183
DB 136 GGCTGGAGTGGATCGGTGATCTATACAGTGGCAACACCTACAGACCCCTGTCCTCA 195

QY 184 AAGAGTCGAGTTACCATGTCCAGTAGACAGTCTTAAGAACCCATTCTCCCTGAGGTGAGC 243
DB 196 AAGAGTCGAGTTACCATGTCCAGTAGACAGTCTTAAGAACCCATTCTCCCTGAGGTGAGC 255

QY 244 TCTGTGACTCCCGGACAGCGCGTGTATTACTGTGCGA-----GGTCAGAT 291
DB 256 TCTGTGACTCCCGGACAGCGCGTGTATTACTGTGCGA-----GGTCAGAT 315

QY 292 GGTGACATTTGGACAACCTGGGCGCAGGGAACCTGTCACTGTCCTCA 342
DB 316 TACTACGGTATGACGCTCTGGGCGCAGGGAACCTGTCACTGTCCTCA 366

RESULT 14
US-09-014-880-9
Sequence 9, Application US/09014880
Patent No. 5990297
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA et al.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
TITLE OF INVENTION: BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,880
FILING DATE: January 28, 1998
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/450,578
FILING DATE: May 25, 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/905,534

OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,363
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:

STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:

TISSUE TYPE:
CELL TYPE: Hybridoma producing human antibody 1-3-1

CELL LINE:
ORGANELLE:

IMMEDIATE SOURCE:
LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-08-450-363-9

Query Match 70.7%; Score 241.8; DB 4; Length 366;

Best Local Similarity 83.2%; Pred. No. 6.7e-68;

Matches 292; Conservative 0; Mismatches 47; Indels 12; Gaps 1;

Qy 4 GAGTCTGCCCGCAGGACTGGTGAAGCCCTTCACAGACCCCTGTCCTCCTCAGCTGCTCTCT 63

Db 16 GAGTCCGGCCCGCAGGACTGGTGAAGCCCTTCGGAGACCCCTGTCCTCCTCAGCTGCTCTCT 75

Qy 64 GTGGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 123
Db 76 GTGGCTCCATCCGAGTGGTGTATTACTGGAGTTGGATCCGCCAGCGTCCAGGGAAG 135
Qy 124 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTACACACCCGTCCTC 183
Db 136 GGCCTGGAGTGGATCGGGTACATCTATCAGTGGCAACACCTACACACCCGTCCTC 195
Qy 184 AAGAGTCGAGTTCACCATATCCGTAGACACCGTCCAGAACCCAGTTCCTCCCTGAGGCTGAGC 243
Db 196 AAGAGTCGAGTTCACCATATCCGTAGACACCGTCCAGAACCCAGTTCCTCCCTGAGGCTGAGC 255
Qy 244 TCTGTGACTGCCCGGACACGCGGTGTTACTGTGCGA-----GGTCAGAT 291
Db 256 TCTGTGACTGCCCGGACACGCGGTGTTACTGTGCGA-----GGTCAGAT 315
Qy 292 GGTACACTTTGGACAACTGGGGCCAGGGAACCGTCCAGCGTCTCCCTCA 342
Db 316 TACTACGGTATGGACGCTCTGGGGCCAGGGAACCGTCCAGCGTCTCCCTCA 366

Search completed: August 13, 2004, 07:18:08

Job time : 49.3636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1368.2 Seconds
(without alignments)
10073.859 Million cell updates/sec

Title: US-10-027-725A-4
Perfect score: 318
Sequence: 1 gagctcaactcagttccatc.....ccaaagtgagatcaaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
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- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
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- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
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- 29: em_vl.*
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- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	318	100.0	318	9	HSA458379	AJ458379 Homo sapi
2	290.8	91.4	322	9	HUMIGHGD	L03142 Homo sapien
3	290.8	91.4	326	9	HUMIGHGY	L03160 Homo sapien
4	289.2	90.9	796	9	AB064138	AB064138 Homo sapi
5	287.6	90.4	321	6	AR161027	AR161027 Sequence
6	286.6	90.1	324	9	AB063929	AB063929 Homo sapi
7	286.6	90.1	828	9	AB064098	AB064098 Homo sapi
8	286.6	90.1	828	9	AB064098	AB064098 Homo sapi
9	286.6	90.1	828	9	AB064098	AB064098 Homo sapi
10	284.4	89.4	324	9	HUMIGHHC	L03184 Homo sapien
11	284.4	89.4	324	9	HUMIGHHC	AF453186 Synthetic
12	282.8	88.9	324	9	AB063932	AB063932 Homo sapi
13	282.8	88.7	321	9	AY240163	AY240163 Homo sapi
14	281.8	88.6	324	9	AB095281	AB095281 Homo sapi
15	281.2	88.4	321	6	AR160973	AR160973 Sequence
16	281.2	88.4	321	6	AR160980	AR160980 Sequence
17	281.2	88.4	321	6	AR161046	AR161046 Sequence
18	281.2	88.4	321	9	HSIGVKL10	X73860 H. sapiens m
19	281.2	88.4	711	12	HSIGVKL31	X95750 Synthetic c
20	280.4	88.2	321	6	E12913	E12913 Human cDNA
21	280.2	88.1	316	9	HUMIGHHS	L03178 Homo sapien
22	280.2	88.1	387	12	AF453148	AF453148 Synthetic
23	279.6	87.9	321	6	AR160978	AR160978 Sequence
24	279.6	87.9	321	6	AR160984	AR160984 Sequence
25	279.6	87.9	321	6	AR161049	AR161049 Sequence
26	279.6	87.9	321	6	AR161050	AR161050 Sequence
27	279.6	87.9	348	9	HSA308458	AJ308458 Homo sapi
28	278.6	87.6	324	9	HSA399875	AJ399875 Homo sapi
29	278.6	87.6	324	9	HSA496511	AJ496511 Homo sapi
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31	278.2	87.5	318	9	AF103519	AF103519 Homo sapi
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33	278.2	87.5	318	12	AF044458	AF044458 Synthetic
34	278.2	87.5	318	12	AF044458	AF044458 Synthetic
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36	277.6	87.3	324	6	BD187175	BD187175 Human-typ
37	277.6	87.3	333	6	BD097236	BD097236 A therape
38	277.6	87.3	346	9	HSG1B61GK	X94431 H. sapiens r
39	277.6	87.3	900	6	BD097240	BD097240 A therape
40	277.2	87.2	314	9	AY062338	AY062338 Homo sapi
41	277.2	87.2	321	9	AY240165	AY240165 Homo sapi
42	277.2	87.2	450	9	AF103775	AF103775 Homo sapi
43	277.2	87.2	450	9	AF103775	AF103775 Homo sapi
44	277.2	87.2	324	9	AB063930	AB063930 Homo sapi
45	277.2	87.2	324	9	AF035037	AF035037 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS HSA458379 318 bp mRNA linear PRI 30-APR-2002
DEFINITION Homo sapiens partial mRNA for immunoglobulin kappa light chain
variable region (IGKV gene), clone 94.
ACCESSION AJ458379
VERSION AJ458379.1 GI:20387057
KEYWORDS IGKV gene; immunoglobulin kappa; light chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
Valent,P., Kraft,D. and Valenta,R.

TITLE Conversion of grass allergen-specific human IgE into a protective
IgG1 antibody
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 318)
AUTHORS Flicker, S.
TITLE Direct Submission
JOURNAL Submitted (24-APR-2002) Flicker S., Department of Pathophysiology,
General Hospital of Vienna, 3Q, Waehringer Guertel 18-20, A-1090
Vienna, AUSTRIA

FEATURES

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Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 TTTGCAAGTTACTACTGTCAAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 300
Db 241 TTTGCAAGTTACTACTGTCAAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 300

QY 301 AAGGTGGAGATCAAAACGA 318
Db 301 AAGGTGGAGATCAAAACGA 318

RESULT 2

HUMIGHGD

LOCUS

DEFINITION Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
(IGHV) mRNA, partial cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

322 bp mRNA linear PRI 03-MAY-2000

L03142

L03142.1 GI:185377

Homo sapiens (human)

Homo sapiens

326 bp mRNA linear PRI 03-MAY-2000

L03160

L03160.1 GI:185395

Homo sapiens

Homo sapiens

REFERENCE
AUTHORS Collet, T.A., Roben, P., O'Kennedy, R., Barbas, C.F. III, Burton, D.R.
and Lerner, R.A.
TITLE A binary plasmid system for shuffling combinatorial antibody
libraries
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE 93066172
PUBMED 1438192

FEATURES

source

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QY 181 AGTGGCAGTGGATATGGACAGACTTCACTCTCACCATCAGAGTCTGCAGCTGAAGAT 240
Db 181 AGTGGCAGTGGATATGGACAGACTTCACTCTCACCATCAGAGTCTGCAGCTGAAGAT 240

QY 241 TTTGCAAGTTACTACTGTCAAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 300
Db 241 TTTGCAAGTTACTACTGTCAAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 300

QY 301 AAGGTGGAGATCAAAACGA 318
Db 301 AAGGTGGAGATCAAAACGA 318

RESULT 3

HUMIGHGY

LOCUS

DEFINITION

ACCESSION

VERSION

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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
              Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 326)
AUTHORS      Collet, T.A.; Roben, P., O'Kennedy, R., Barbas, C.F. III, Burton, D.R.
              and Lerner, R.A.
TITLE        A binary plasmid system for shuffling combinatorial antibody
              libraries
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
MEDLINE      93066172
PUBMED       1438192
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Db  301 AAGGTGGAGATCAACAGA 318
RESULT 4
AB064138
LOCUS      AB064138
DEFINITION Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ

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region, partial cds, clone:K97.
AB064138
VERSION      GI:21669482
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
            Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
            Miura, K. and Kurosawa, Y.
TITLE      Construction and characterization of antibody libraries: Isolation
            of therapeutic human antibodies and application to functional
            genomics
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 796)
AUTHORS     Kurosawa, Y.
TITLE      Direct Submission
JOURNAL     Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University,
            Kutsukake-cho, Toyooka 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
            Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
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Qy  181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGTGTGCAAGCTGAAGAT 240
Db  253 AGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGAGTGTGCAAGCTGAAGAT 312
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RESULT 5
LOCUS   AR161027          321 bp      DNA          linear      PAT 17-OCT-2001
DEFINITION Sequence 199 from patent US 6255455.
ACCESSION AR161027
VERSION   AR161027.1  GI:16226382
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 321)
AUTHORS Siegel,D.L.
TITLE    Rh(D)-binding proteins and magnetically activated cell sorting
          method for production thereof
JOURNAL Patent: US 6255455-A 199 03-JUL-2001;
FEATURES Location/Qualifiers
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Best Local Similarity 94.0%; Pred. No. 2e-83;
Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY      181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTCAGCCTGAAGAT 240
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QY      301 AAGGTGGAGATCAAAACGA 318
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RESULT 6
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DEFINITION Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
ACCESSION AB063929
VERSION   AB063929.1  GI:21669064
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
          Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,

Miura,K. and Kurosawa,Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
Unpublished
2 (bases 1 to 324)
Kurosawa,Y.
Direct Submission
Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
Please visit our web site
URL:http://www.fujita-hu.ac.jp/immunity/.
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ORIGIN
Query Match      90.1%; Score 286.6; DB 9; Length 324;
Best Local Similarity 94.0%; Pred. No. 4.2e-83;
Matches 298; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      2 AGTCATCTCAGTCTCCATCTCCCTGCTGTCATCTGTGGGAGACAGATCACCATCAGT 61
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RESULT 7
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DEFINITION Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
ACCESSION AB064098
VERSION   AB064098.1  GI:21669402
KEYWORDS .

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SOURCE Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
 Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
 Miura, K. and Kurosawa, Y.
 TITLE Construction and characterization of antibody libraries: isolation
 of therapeutic human antibodies and application to functional
 genomics
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 828)
 AUTHORS Kurosawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
 Comprehensive Medical Science, Fujita Health University;
 Kutsukake-cho, Toyosake 470-1192, Japan
 (E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)
 COMMENT Please visit our web site
 URL: http://www.fujita-hu.ac.jp/immunity/
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Qy 302 AGGTGGAGATCAACGA 318
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 DEFINITION H.sapiens mRNA for Ig kappa light chain variable region
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 ACCESSION X73855
 VERSION X73855.1 GI:516316
 KEYWORDS autoantibody; Ig J-segment; Ig kappa light chain; Ig subgroup 1; Ig
 variable region; immunoglobulin.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 321)
 AUTHORS Hexham, J.M., Furmaniak, J., Pegg, C., Burton, D.R. and Smith, B.R.
 TITLE Cloning of a human autoimmune response: preparation and sequencing
 of a human anti-thyroglobulin autoantibody using a combinatorial
 approach
 JOURNAL Autoimmunity 12 (2), 135-141 (1992)
 MEDLINE 92314301
 PUBMED 1617110
 REFERENCE 2 (bases 1 to 321)
 AUTHORS Hexham, J.M., Partridge, L.J., Furmaniak, J., Peterson, V.B.,
 Colls, J.C., Pegg, C., Rees Smith, B. and Burton, D.R.
 TITLE Cloning and characterisation of TPO autoantibodies using
 combinatorial phage display libraries
 JOURNAL Autoimmunity 17 (3), 167-179 (1994)
 MEDLINE 95035699
 PUBMED 7524700
 REFERENCE 3
 AUTHORS Hexham, J.M., Partridge, L.J., Furmaniak, J., Petersen, V.B.,
 Colls, J.C., Pegg, C.A.S., Rees-Smith, B. and Burton, D.R.,
 TITLE Probing the human anti-thyroid peroxidase repertoire of a
 Hashimoto's thyroiditis patient using combinatorial phage display
 libraries
 JOURNAL Eur. J. Immunol.
 REFERENCE 4 (bases 1 to 321)
 AUTHORS Hexham, J.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-1993) J. Hexham, Univ. of Sheffield, Dept. of
 Mol. Biology and Biotechnology, P. O. Box 594, Firth Court, Western
 Bank, Sheffield S10 2UH, UK
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 REFERENCE 1 (bases 1 to 328)
 AUTHORS Collet,T.A., Roben,P., O'Kennedy,R., Barbas,C.F. III, Burton,D.R.
 and Lerner,R.A.
 TITLE A binary plasmid system for shuffling combinatorial antibody
 libraries
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
 MEDLINE 93066172
 PUBMED 1438192

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RESULT 10 AB095286 324 bp mRNA linear PRI 25-JUL-2003
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REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Tachibana,H., Watanabe,K., Cheng,X.J., Teukamoto,H., Kaneda,Y.,
 Takeuchi,T., Ihara,S. and Petri Jr,W.A. Jr.
 TITLE VH3 Gene Usage in Neutralizing Human Antibodies Specific for the
 Entamoeba histolytica Gal/GalNAc Lectin Heavy Subunit
 JOURNAL Infect. Immun. 71 (8), 4313-4319 (2003)
 PUBMED 12874307
 REFERENCE 2 (bases 1 to 324)
 AUTHORS Tachibana,H.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-2002) Hiroshi Tachibana, Tokai University School
 of Medicine, Department of Infectious Diseases, Bohseidai, Isehara,
 Kanagawa 259-1193, Japan (E-mail:htachiba@is.icc.u-tokai.ac.jp,
 Tel:81-463-93-1121(ex.2603), Fax:81-463-95-5450)

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ACCESSION  AR160973
VERSION     AR160973.1  GI:16226189
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 321)
AUTHORS    Siegel,D.I.
TITLE       Rh(D)-binding proteins and magnetically activated cell sorting
            method for production thereof
JOURNAL     Patent: US 6255455-A 102 03-JUL-2001;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 1864.96 Seconds
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	275.4	86.6	493	10	AW405753	AW405753 UI-HF-BL0
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8	275.4	86.6	799	14	CB984750	CB984750 AGENCOURT
9	275.4	86.6	807	14	CB958380	CB958380 AGENCOURT
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37	269	84.6	855	14	CB995312	CB995312 AGENCOURT
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39	269	84.6	1084	14	CB986592	CB986592 AGENCOURT
40	267.6	84.2	471	14	CD706522	CD706522 EST23049
41	267.6	84.2	1012	13	BX397738	BX397738 BX397738
42	267.4	84.1	431	10	AW406886	AW406886 UI-HF-BL0
43	267.4	84.1	743	14	CB957909	CB957909 AGENCOURT
44	267.4	84.1	837	14	CB984807	CB984807 AGENCOURT
45	265.8	83.6	725	14	CB987519	CB987519 AGENCOURT

ALIGNMENTS

RESULT 1
AW405752
LOCUS
DEFINITION
UI-HF-BL0-abp-a-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3057288 5', mRNA sequence.
ACCESSION
AW405752
VERSION
AW405752.1 GI:6924809
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 447)
NIH-MGC <http://mgc.ncl.nih.gov/>
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES		Location/Qualifiers	
source		1. .447	
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		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
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		/tissue_type="lymph"	
		/cell_type="germinal center B cells"	
		/cell_line="MGC85"	
		/lab_host="DH10B (LTI)"	
		/clone_lib="NIH MGC 37"	
		/note="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."	
ORIGIN			
Query Match		88.1%; Score 280.2; DB 10; Length 447;	
Best Local Similarity		92.7%; Pred. No. 3.3e-78;	
Matches 294; Conservative		0; Mismatches 23; Indels 0; Gaps 0;	
QY	2	AGCTCACTCAGTCTCCATCTCCCTGCTGTGATCTGTGGGAGACAGATCAACATCACTT	61
Db	90	AGATGACCCAGTCTCCATCTCCCTGCTGTGATCTGTAGGAGACAGATCAACATCACTT	149
QY	62	GCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATAAACAGGGAAG	121
Db	150	GCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCAGACAGGGAAG	209
QY	122	CCCCTAAGCTCTGATCTGATCGATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTCA	181
Db	210	CCCCTAAGCTCTGATCTGATCGATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTCA	269
QY	182	GTGCAGTGGATATCGGACAGATTCATCTCACCATCAGCAGTCTGAGCTCAAGATT	241
Db	270	GTGCAGTGGATATCGGACAGATTCATCTCACCATCAGCAGTCTGAGCTCAAGATT	329
QY	242	TTGCAAGTTACTACTGTCAAGAGTCTCAGTGCCTCTGATCTTTCGCGGAGGACCA	301
Db	330	TTGCAAGTTACTACTGTCAAGAGTCTCAGTGCCTCTGATCTTTCGCGGAGGACCA	389
QY	302	AGGTGGAGATCAACCA 318	
Db	390	AGGTGGAGATCAACCA 406	
RESULT 2			
AW407904		422 bp mRNA linear EST 16-FEB-2000	
LOCUS		UI-HF-BL0-add-a-01-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone	
DEFINITION		IMAGE:3061128 5', mRNA sequence.	
ACCESSION		AW407904	
VERSION		AW407904.1 GI:6926961	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1 (bases 1 to 422)	
AUTHORS		NIH-MGC http://mgi.nci.nih.gov/ .	
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ LNL.nl : www.bio.llnl.gov/bbrp/image/image.html	

FEATURES		Location/Qualifiers	
source		1. .447	
		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:3057288"	
		/tissue_type="lymph"	
		/cell_type="germinal center B cells"	
		/cell_line="MGC85"	
		/lab_host="DH10B (LTI)"	
		/clone_lib="NIH MGC 37"	
		/note="Vector: p77T3-Pac; Site 1: NotI; Site 2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."	
ORIGIN			
Query Match		88.1%; Score 280.2; DB 10; Length 447;	
Best Local Similarity		92.7%; Pred. No. 3.3e-78;	
Matches 294; Conservative		0; Mismatches 23; Indels 0; Gaps 0;	
QY	2	AGCTCACTCAGTCTCCATCTCCCTGCTGTGATCTGTGGGAGACAGATCAACATCACTT	61
Db	90	AGATGACCCAGTCTCCATCTCCCTGCTGTGATCTGTAGGAGACAGATCAACATCACTT	149
QY	62	GCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCATAAACAGGGAAG	121
Db	150	GCCGGGCAAGTCAGAGATTAAACCTATTAAATTGGTATCAGCAGACAGGGAAG	209
QY	122	CCCCTAAGCTCTGATCTGATCGATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTCA	181
Db	210	CCCCTAAGCTCTGATCTGATCGATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTCA	269
QY	182	GTGCAGTGGATATCGGACAGATTCATCTCACCATCAGCAGTCTGAGCTCAAGATT	241
Db	270	GTGCAGTGGATATCGGACAGATTCATCTCACCATCAGCAGTCTGAGCTCAAGATT	329
QY	242	TTGCAAGTTACTACTGTCAAGAGTCTCAGTGCCTCTGATCTTTCGCGGAGGACCA	301
Db	330	TTGCAAGTTACTACTGTCAAGAGTCTCAGTGCCTCTGATCTTTCGCGGAGGACCA	389
QY	302	AGGTGGAGATCAACCA 318	
Db	390	AGGTGGAGATCAACCA 406	
RESULT 3			
AW407904		525 bp mRNA linear EST 25-JUN-2003	
LOCUS		EST22455 human nasopharynx Homo sapiens cDNA, mRNA sequence.	
DEFINITION		CD705928	
ACCESSION		CD705928	
VERSION		CD705928.1 GI:32236558	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1 (bases 1 to 525)	
AUTHORS		Liu,X.-O., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.	
TITLE		Transcriptional Gene Expression Profile of Human Nasopharynx	
JOURNAL		Unpublished (2003)	
COMMENT		Contact: Yixin Zeng Cancer Center Sun Yat-sen University 651 Dongfeng Road East, Guangzhou 510060, China Tel: 86-1380-9770-743 Fax: 86-20-8775-4506 Email: yxzeng@gzsums.edu.cn	

FEATURES source
1. .525
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"

ORIGIN

Query Match      87.6%; Score 278.6; DB 14; Length 525;
Best Local Similarity 92.4%; Pred. No. 1.2e-77;
Matches 293; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY  2 AGCTCACTCAGTCTCCATCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCAGTT 61
Db  124 AGATGACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCATT 183
QY  62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACACGGGAAAG 121
Db  184 GCCGGGCAAGTCAGAGCAATAGCAGCTATTAAATTGGTATCAGCATAAACACGGGAAAG 243
QY  122 CCCCTAAGCTCTGATCTATGCTGATCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCAGTTCA 181
Db  244 CCCCTAAGCTCTGATCTATGCTGATCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCAGTTCA 303
QY  182 GTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCGAGCTCAAGATT 241
Db  304 GTGGCAGTGGATCTGGGACAGATTTCATCTCGCCATCAGCAGTCGAGCTCAAGATT 363
QY  242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
Db  364 TTGCAACTTACCCTGTCAACAGAGTTACAGTACGCGGTACACTTTTGGCCAGGGGACCA 423
QY  302 AGGTGGAGATCAACGA 318
Db  424 ACCTGGAGATCAACGA 440

RESULT 4
CD690145
LOCUS      624 bp mRNA linear EST 25-JUN-2003
DEFINITION human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION  CD690145
VERSION     CD690145.1 GI:32210615
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 624)
AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL   Unpublished (2003)
COMMENT   Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 Dongfeng Road East, Guangzhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES   Location/Qualifiers
            1..624
            /organism="Homo sapiens"
            /mol_type="mRNA"
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            /tissue_type="normal nasopharynx"
            /clone_lib="human nasopharynx"
            /note="ESTs generated from a normal nasopharynx cDNA
            library from southern Chinese"

ORIGIN

Query Match      87.6%; Score 278.6; DB 14; Length 624;

Best Local Similarity 92.4%; Pred. No. 1.2e-77;
Matches 293; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY  2 AGCTCACTCAGTCTCCATCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCAGTT 61
Db  121 AGATGACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCATT 180
QY  62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTGGTATCAGCATAAACACGGGAAAG 121
Db  181 GCCGGGCAAGTCAGAGCAATAGCAGCTATTAAATTGGTATCAGCATAAACACGGGAAAG 240
QY  122 CCCCTAAGCTCTGATCTATGCTGATCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCAGTTCA 181
Db  241 CCCCTAAGCTCTGATCTATGCTGATCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCAGTTCA 300
QY  182 GTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCGAGCTCAAGATT 241
Db  301 GTGGCAGTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCGAGCTCAAGATT 360
QY  242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
Db  361 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAGAACTTTTGGCCAGGGGACCA 420
QY  302 AGGTGGAGATCAACGA 318
Db  421 AGCTGGAGATCAACGA 437

RESULT 5
AW405301
LOCUS      487 bp mRNA linear EST 16-FEB-2000
DEFINITION UT-HP-BLO-ack-b-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3059259 5', mRNA sequence.
ACCESSION  AW405301
VERSION     AW405301.1 GI:6924358
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 487)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs-k@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES   Location/Qualifiers
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
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            /cell_type="germinal center B cells"
            /cell_line="MGC85"
            /lab_host="DH10B (LT1)"
            /clone_lib="NIH_MGC_37"
            /note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
            Constructed from size fractionated cytoplasmic mRNA
            (1.5-2.5kb). Directionally cloned. Cells provided by Louis
            M. Staudt, Ph.D. Library preparation by Maria de Fatima
            Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN
```


C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

```

ORIGIN
Query Match      86.6%; Score 275.4; DB 14; Length 748;
Best Local Similarity 91.8%; Pred. No. 1.6e-76;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy  2 AGCTCACTCAGTCTCCATCCCTCCCTGCTGTCGATCTGTGGGAGACAGAGTCAACATCAGTT 61
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Db 102 AGATGACCCAGTCTCCATCCCTCCCTGCTGTCGATCTGTAGGAGACAGAGTCAACATCAGTT 161
    |||

Qy  62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACACGGGAAAG 121
    |||
Db 162 GCCGGGCAAGTCAGAGAAATTAAGTAGTATTAAATTTGGTATCAGCAGAAACGAGGAAAG 221
    |||

Qy 122 CCCCTAAGCTCCTGATCTGATCTGCATCCAGTTTGCAGAGTGGGTCCTCCATCAAGTTTCA 181
    |||
Db 222 CCCCTAAGCTCCTGATCTGATCTGCATCCAGTTTGCAGAGTGGGTCCTCCATCAAGTTTCA 281
    |||

Qy 182 GTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTCAAGATT 241
    |||
Db 282 GTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTCAAGATT 341
    |||

Qy 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
    |||
Db 342 CTGCAACTTACTACTGTCAAGAGAGTCAAGTACCCCTTGGACTTTTGGCCAGGGGACCA 401
    |||

Qy 302 AGTGGAGATCAAAACGA 318
    |||
Db 402 AGTGGAGATCAAAACGA 418
    |||

RESULT 8
CB984750      799 bp mRNA linear EST 01-MAY-2003
LOCUS
DEFINITION
AGENCOURT_13574990 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30326373 5', mRNA sequence.
CB984750
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 799)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM133 row: k column: 22
High quality sequence stop: 412.
Location/Qualifiers
1. 799
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30326373"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site:1:
SfiI (ggccattatggcc); Site:2: SfiI (ggcgccctcgcc);"

FEATURES
source
1. 799
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30326373"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site:1:
SfiI (ggccattatggcc); Site:2: SfiI (ggcgccctcgcc);"

ORIGIN
Query Match      86.6%; Score 275.4; DB 14; Length 799;
Best Local Similarity 91.8%; Pred. No. 1.6e-76;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy  2 AGCTCACTCAGTCTCCATCCCTCCCTGCTGTCGATCTGTGGGAGACAGAGTCAACATCAGTT 61
    |||
Db 101 AGATGACCCAGTCTCCATCCCTCCCTGCTGTCGATCTGTAGGAGACAGAGTCAACATCAGTT 160
    |||

Qy  62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACACGGGAAAG 121
    |||
Db 161 GCCGGGCAAGTCAGAGAAATTAAGTAGTATTAAATTTGGTATCAGCATAAACACGGGAAAG 220
    |||

Qy 122 CCCCTAAGCTCCTGATCTGATCTGCATCCAGTTTGCAGAGTGGGTCCTCCATCAAGTTTCA 181
    |||
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Qy 182 GTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTCAAGATT 241
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Qy 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
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Db 341 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 400
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Qy 302 AGTGGAGATCAAAACGA 318
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Db 401 AGTGGAGATCAAAACGA 417
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RESULT 9
CB958380      807 bp mRNA linear EST 29-APR-2003
LOCUS
DEFINITION
AGENCOURT_13666601 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30353194 5', mRNA sequence.
CB958380
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 807)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM153 row: i column: 11
High quality sequence stop: 532.
Location/Qualifiers
1. 807
/organism="Homo sapiens"
/mol_type="mRNA"

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Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGGCGCAGATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

/db_xref="taxon:9606"
/clone="IMAGE:30353194"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:4576560"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 86.6%; Score 275.4; DB 14; Length 807;
Best Local Similarity 91.8%; Pred. No. 1.6e-76;
Matches 291; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 2 AGCTCACTCAGTCTCCATCCCTCTGTCATCTGTGGGACAGAGTCACCATCAGTT 61
DB 101 AGATGACCCAGTCTCCATCCCTCTGTCATCTGTGGGACAGAGTCACCATCAGTT 160
QY 62 GCCGGGCAAGTCAGAGATTAAACCTATTTAAATGGTATCAGCATTAACAGGGAAG 121
DB 161 GCCGGGCAAGTCAGAGATTAAACCTATTTAAATGGTATCAGCATTAACAGGGAAG 220
QY 122 CCCCTAAGCTCTGATCTGTCATCTGTCATCTGTGGGACAGAGTCACCATCAGTTCA 181
DB 221 CCCCTAAGCTCTGATCTGTCATCTGTCATCTGTGGGACAGAGTCACCATCAGTTCA 280
QY 182 GTGGCAGTGGATATGGGACAGAGTTCCTCTCACCATCAGCAGTCTGCAGCTCGAAGATT 241
DB 281 GTGGCAGTGGTCTGGGACAGAGTTCCTCTCACCATCAGCAGTCTGCAGCTCGAAGATT 340
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTCTGTCATCTTGGCCAGGGGACCA 301
DB 341 TTGCAAGTTACTACTGTCAAGAGAGTTCAGTACCCCTGTCTCACTTTGGCCAGGGGACCA 400
QY 302 AGGTGGAGATCAAAACA 318
DB 401 AGCTGGAGATCAAAACA 417

RESULT 10

BG341239
LOCUS BG341239
DEFINITION 602463904F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576560 5', mRNA sequence.

ACCESSION BG341239

VERSION BG341239.1 GI:13147677

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLC1289 row: h column: 01
High quality sequence stop: 732.

FEATURES
source Location/Qualifiers

1..921
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:4576560"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 86.4%; Score 274.6; DB 12; Length 921;
Best Local Similarity 93.7%; Pred. No. 3.2e-76;
Matches 297; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

QY 2 AGCTCACTCAGTCTCCATCCCTCTGTCATCTGTGGGACAGAGTCACCATCAGTT 61
DB 88 AGATGACCCAGTCTCCATCCCTCTGTCATCTGTGGGACAGAGTCACCATCAGTT 147
QY 62 GCCGGGCAAGTCAGAGATTAAACCTATTTAAATGGTATCAGCATTAACAGGGAAG 121
DB 148 GCCGGGCAAGTCAGAGATTAAACCTATTTAAATGGTATCAGCATTAACAGGGAAG 206
QY 122 CCCCTAAGCTCTGATCTGTCATCTGTCATCTGTGGGACAGAGTCACCATCAGTTCA 181
DB 207 CCCCTAAGCTCTGATCTGTCATCTGTCATCTGTGGGACAGAGTCACCATCAGTTCA 266
QY 182 GTGGCAGTGGATATGGGACAGAGTTCCTCTCACCATCAGCAGTCTGCAGCTCGAAGATT 241
DB 267 GTGGCAGTGGATATGGGACAGAGTTCCTCTCACCATCAGCAGTCTGCAGCTCGAAGATT 326
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTCTGTCATCTTGGCCAGGGGACCA 301
DB 327 TTGCAAGTTACTACTGTCAAGAGAGTTCAGTACCCCTGTCTCACTTTGGCCAGGGGACCA 386
QY 302 AGGTGGAGATCAAAACA 318
DB 387 AGCTGGAGATCAAAACA 403

RESULT 11

BX397739

LOCUS BX397739

DEFINITION BX397739 Homo sapiens PLACENTA COT 23-NORMALIZED Homo sapiens cDNA clone CS01041YPO6 5-PRIME, mRNA sequence.

ACCESSION BX397739

VERSION BX397739.1 GI:30617375

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 BVRY cedex - France

Email: seqrefgenoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 1696.r For

more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI041DH03QP1&cluster=1696.r>. Contact : Feng liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI041DH03QP1.

FEATURES

source

1. .498
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 86.1%; Score 273.8; DB 14; Length 498;
Best Local Similarity 91.5%; Pred. No. 3.9e-76;
Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Qy 2 AGCTCACTCAGTCCCATCCCTCTGTCATCTGTGGGAGACAGAGTCACCATCAGTT 61
Db 134 AGATGACCCAGTCCCATCCCTCTGTCATCTGTGGGAGACAGAGTCACCATCATT 193
Qy 62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCGGAAAG 121
Db 194 GCCGGGCAAGTCAGGGCATGAGCACCTATTAAATTTGGTATCAGCAGAAACCGGAAAG 253
Qy 122 CCCCTAAGCTCCTGATCTATGTCATCCAGTTTGGAAAGTGGGGTCCCATCAAGTTCA 181
Db 254 CCCCTAAGCTCCTGATCTGTCATCCAGTTTGGAAAGTGGGGTCCCATCAAGTTCA 313
Qy 182 GTGGCAGTGGATATGGGACAGACTTCACTCTCCACATCAGCAGTCTGCAGCCTCAAGATT 241
Db 314 GTGGCAGTGGATCTGGGACAGATTTCATCTCCACATCAGCAGTCTGCACCTCAAGATT 373
Qy 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTCGTACACTTTGGCCAGGGGACCA 301
Db 374 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTCGTACACTTTGGCCAGGGGACCA 433
Qy 302 AGGTGGAGATCAACGA 318
Db 434 AGGTGGAAATCAACGA 450

RESULT 13

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .498

/organism="Homo sapiens"

/db_xref="taxon:9606"

/tissue_type="normal nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI041DH03QP1&cluster=1696.r>. Contact : Feng liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI041DH03QP1.

FEATURES

source

1. .498
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 86.2%; Score 274; DB 13; Length 1067;
Best Local Similarity 93.4%; Pred. No. 5.5e-76;
Matches 297; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
Qy 2 AGCTCACTCAGTCCCATCCCTCTGTCATCTGTGGGAGACAGAGTCACCATCAGTT 61
Db 129 AGATGACCCAGTCCCATCCCTCTGTCATCTGTGGGAGACAGAGTCACCATCATT 188
Qy 62 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCGGAAAG 121
Db 189 GCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCGGAAAG 248
Qy 122 CCCCTAAGCTCCTGATCTATGTCATCCAGTTTGGAAAGTGGGGTCCCATCAAGTTCA 181
Db 249 CCCCTAAGCTCCTGATCTATGTCATCCAGTTTGGAAAGTGGGGTCCCATCAAGTTCA 308
Qy 182 GTGGCAGTGGATATGGGACAGACTTCACTCTCCACATCAGCAGTCTGCAGCCTCAAGATT 241
Db 309 GTGGCAGTGGATCTGGGACAGATTTCATCTCCACATCAGCAGTCTGCACCTCAAGATT 368
Qy 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTCGTACACTTTGGCCAGGGGACC 300
Db 369 ATTGCAACTTACTACTGTCAAGAGAGTCTCAGTGGCTCGTACACTTTGGCCAGGGGACC 428
Qy 301 AAGGTGGAGATCAACGA 318
Db 429 AAGCTGGAGATCAACGA 446

RESULT 12

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .498

/organism="Homo sapiens"

/db_xref="taxon:9606"

/tissue_type="normal nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Query Match	86.1%	Score	273.8	DB	14	Length	499
Best Local Similarity	91.5%	Pred. No.	3.9e-76				
Matches	290	Conservative	0	Mismatches	27	Indels	0
Gaps	0						
Qy	2	AGCTCACTCAGTCTCCATCCTCCCTGTCGTGATCTGTGGGAGACAGAGTCACCATCAGTT	61				
Db	137	AGATGACCCAGTCTCCATCCTCCCTGTCGTGATCTGTAGGAGACAGAGTCAGATCACTT	196				
Qy	62	GCCTGGCAAGTCAGAGAAATTAACACCTATTTAAATTTGGTATCAGCATAAACCCAGGGAAG	121				
Db	197	GCCTGGCAAGTCAGAGCATTTAGCAACTATTTAAATTTGGTATCAGCAGAAACCCAGGGAAG	256				
Qy	122	CCCCTAAGTCTCTGATCTATGCTGCATCCAGTCTTGCAAAAGTGGGGTCCCATCAAGGTTCA	181				
Db	257	CCCCTAAGTCTCTGATCTATGCTGCATCCAGTCTTGCAAAAGTGGGGTCCCATCAAGGTTCA	316				
Qy	182	GTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGATT	241				
Db	317	GTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCACACCTGAGATT	376				
Qy	242	TTGCAAGTTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTATACATTTTGGCCAGGGGACCA	301				
Db	377	TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGCTCACTTTTCGGCGGGGACCA	436				
Qy	302	AGTGGAGATCAAAACGA	318				
Db	437	CGTGGAGATCAGACGA	453				

RESULT	14
AWA04714	
LOCUS	
DEFINITION	608 bp mRNA linear EST 16-FEB-2000 UT-HF-BLO-acd-C-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
ACCSSION	UWAGH:3058580 5', mRNA sequence.
VERSION	AWA04714
KEYWORDS	AWA04714.1 GI:6923771
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL	1 (bases 1 to 608)
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.

ORIGIN

Query Match	86.1%;	Score 273.8;	DB 10;	Length 608;
Best Local Similarity	91.5%;	Pred. No. 4.5e-76;		
Matches 290;	Conservative 0;	Mismatches 27;	Indels 0;	Gaps 0;
Qy 2	AGCTCACTCAGTCTCCATCCTCCCTGCTCTGTCATCTCTGGGAGACAGAGTCACCATCAGTT	61		
Db 49	AGATGACCCAGTCTCCATCCTCCCTGCTGCATCTCTAGGAGCAGAGTCACCATCACTT	108		
Qy 62	GCCGGGCAAGTCAGAGAAATTAACACCTATTTAAATTGGTATCAGCATATAAACCGGGAAG	121		
Db 109	GCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAATCAGGGAAG	168		
Qy 122	CCCTTAAGCTCTGATCTATGCTGCATCAGTTTGCAAAAGTGGGTCCTCATCAAGTTCA	191		
Db 169	CCCTTAACCTCTGATCTATGCTGCATCCAGTTTGCAAAATGGGTCCTCATCAAGTTCA	228		
Qy 182	GTGGCAGTGATATGGAGAGAGCTTCACCTCTCACCATCAGCAGCTCTGCAGCCTGGAAGATT	241		
Db 229	GTGGCAGTGGATCTGGGACAGATTTCACCTTCACCATCAGCAGCTCTGCACCTGAAGATT	288		
Qy 242	TTGCAAGTTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA	301		
Db 289	TTGCAACTTACTTCTGTGACGACAGTTTCACTACCCCGTACAGTTTTTGGCCAGGGGACCA	348		
Qy 302	AGTGGAGATCAAAACGA	318		
Db 349	GACTGGAGATCAAAACGA	365		

RESULT	15
LOCUS	CB959008
DEFINITION	AGENCOURT I3664954 NIH MGC 184 Homo sapiens cDNA clone IMAGE:30354121 5' , mRNA sequence.
VERSION	CB959008
KEYWORDS	EST.
SOURCE	Homo sapiens GI:30215124
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 724) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

FEATURES

C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

```
Query Match      86.1%; Score 273.8; DB 14; Length 724;
Best Local Similarity 91.5%; Pred No. 5e-76;
Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 2 AGCTCAGTCTCCATCCCTCTGTCTGTGATCTGTGGGACAGAGTCACCATCAGTT 61
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 97 AGATGACCCAGTCTCCATCCCTCTGTCTGTGATCTGTAGGACAGAGTCACATCACTT 156
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 GCCGGGCAAGTCAGAGAAATTAACACCTATTTAAATTTGGTATCAGCATAAACCAGGAAAG 121
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 157 GCCGGGCAAGTCAGAGCAATTAACAGGTATTTAAATTTGGTATCAGCAGAAACCAGGAAAG 216
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 122 CCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCATCAAGTTCA 181
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 217 CCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCATCAAGTTCA 276
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 182 GTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGATT 241
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGATT 336
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 337 TTGCAACTTACTACTGTCAAGAGAGTTACAGTACCCTCCGACGTTCCGCAAGGGACCA 396
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 302 AGGTGGAGATCAAAACA 318
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 397 AGGTGGAAATCAACGA 413
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: August 13, 2004, 07:13:23
Job time : 1867.96 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 11:40:47 ; Search time 207.182 Seconds
(without alignments)
6520.490 Million cell updates/sec

Title: US-10-027-725A-4
Perfect score: 318
Sequence: 1 gagctcactcagtcctccatc.....ccaaaggtggagatcaaacga 318

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318	100.0	318	6	ABK89640 DNA encod
2	287.6	90.4	321	5	Aah68701 Human ant
3	287.6	90.4	321	8	ACD45365 Anti-Rh(D
4	281.2	88.4	321	5	Aah68720 Human ant
5	281.2	88.4	321	5	Aah68654 Human ant
6	281.2	88.4	321	5	Aah68647 Human ant
7	281.2	88.4	321	8	ACD45311 Anti-Rh(D
8	281.2	88.4	321	8	ACD45318 Anti-Rh(D
9	281.2	88.4	321	8	ACD45384 Anti-Rh(D
10	280.4	88.2	321	2	AAT66781 Anti-canc
11	279.6	87.9	321	5	Aah68723 Human ant
12	279.6	87.9	321	5	Aah68658 Human ant
13	279.6	87.9	321	5	Aah68724 Human ant
14	279.6	87.9	321	5	Aah68652 Human ant
15	279.6	87.9	321	8	ACD45388 Anti-Rh(D
16	279.6	87.9	321	8	ACD45387 Anti-Rh(D
17	279.6	87.9	321	8	ACD45316 Anti-Rh(D
18	279.6	87.9	321	8	ACD45322 Anti-Rh(D
19	277.6	87.3	324	7	AAL52120 Human ant
20	277.6	87.3	333	5	Aah74684 Nucleotid
21	277.6	87.3	333	5	ABT34320 Hepatitis
22	277.6	87.3	720	7	ABT34315 Hepatitis
23	277.6	87.3	900	5	Aah74688 Nucleotid

24	277.6	87.3	900	7	ABT34324 Hepatitis
25	277	87.1	396	2	AAT75423 Human ant
26	276.4	86.9	321	5	Aah68713 Human ant
27	276.4	86.9	321	5	Aah68703 Human ant
28	276.4	86.9	321	8	ACD45377 Anti-Rh(D
29	276.4	86.9	321	8	ACD45367 Anti-Rh(D
30	276.2	86.9	324	5	Aah68657 Human ant
31	276.2	86.9	324	5	Aah68712 Human ant
32	276.2	86.9	324	5	Aah68646 Human ant
33	276.2	86.9	324	8	ACD45321 Anti-Rh(D
34	276.2	86.9	324	8	ACD45376 Anti-Rh(D
35	276.2	86.9	324	8	ACD45310 Anti-Rh(D
36	276	86.8	720	2	AAX36070 DNA encod
37	276	86.8	720	7	ABZ76706 Human ser
38	275.4	86.6	341	2	AAT60119 Coding se
39	275.4	86.6	729	3	AAAL1630 Human imm
40	275.4	86.6	729	6	ABL46009 Humanised
41	274.8	86.4	321	5	Aah68718 Human ant
42	274.8	86.4	321	5	Aah68650 Human ant
43	274.8	86.4	321	8	ACD45382 Anti-Rh(D
44	274.8	86.4	321	8	ACD45314 Anti-Rh(D
45	274.2	86.2	322	6	ABS62720 Anti-IGF-

ALIGNMENTS

RESULT 1

ID	ABK89640	standard; DNA; 318 BP.
XX	ABK89640	
AC	ABK89640;	
XX		
DT	21-OCT-2002	(first entry)
XX		
DE	DNA encoding human Ige Fab clone 94 light chain.	
XX		
KW	Human; fab; ds; gene; antiallergic; vaccine; grass pollen; Phi p 2;	
KW	timothy grass pollen allergen; passive immunotherapy.	
XX		
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
FT	CDS	1..318
FT		/*tag= a
FT		/product= "Fab clone 94 light chain"
FT	misc_feature	7..63
FT		/*tag= b
FT		/note= "FR1 region"
FT	misc_feature	64..96
FT		/*tag= c
FT		/note= "CDR1 region"
FT	misc_feature	97..141
FT		/*tag= d
FT		/note= "FR2 region"
FT	misc_feature	142..162
FT		/*tag= f
FT		/note= "CDR2 region"
FT	misc_feature	163..258
FT		/*tag= g
FT		/note= "FR3 region"
FT	misc_feature	259..285
FT		/*tag= h
FT		/note= "CDR3 region"
XX		
WO	2002053595-A1.	
PD	11-JUL-2002.	
XX		
PF	27-DEC-2001; 2001WO-SE002908.	
XX		
PR	29-DEC-2000; 2000SE-00004892.	
XX		

PA (PHAA) PHARMACIA DIAGNOSTICS AB.
 XX
 PI Flicker S, Steinberger P, Kraft D, Valenta R;
 XX
 DR WPI; 2002-583604/62.
 DR P-PSDB; ABG30448.
 XX
 PT Group 2 allergen-specific immunoglobulins (Ig) E Fabs or IgG comprising
 PT variable region of group 2 allergen specific-human IgE Fabs, useful for
 PT diagnosing or passive immunotherapy of type I allergy, for environmental
 PT allergen detection.
 XX
 PS Disclosure; Page 34; 45pp; English.
 PS
 XX
 CC This invention relates to the DNA and protein sequences of group 2
 CC allergen-specific human IgE Fabs and methods for their use. The proteins
 CC of the invention may have anti-allergic activities and may be used as a
 CC vaccine or an inhibitor of binding of grass pollen allergic patient's IgE
 CC antibodies to Phi p 2 (a major timothy grass pollen allergen). The group
 CC 2 allergen-specific fabs of the invention may be useful for environmental
 CC allergen detection and for standardisation of allergen extracts. The fabs
 CC - or a vaccine against a type I allergy is useful for passive
 CC immunotherapy of type I allergy, it is also useful for diagnosing a type
 CC I allergy. The allergen-specific fabs of the invention are useful for
 CC inter alia, diagnosis, therapy and prevention of type I allergy. They are
 CC also useful for identification of group 2 allergen-containing pollen and
 CC may be used for blocking the binding of grass pollen allergic patients
 CC IgE antibodies to Phi p 2. The present sequence represents the DNA
 CC encoding the human IgG fab, clone 94 light chain protein of the invention
 XX
 SQ Sequence 318 BP; 84 A; 81 C; 77 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 318; DB 6; Length 318;
 Best Local Similarity 100.0%; Pred. No. 7.4e-91;
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGCTCACATCAGTCTCCCTCCCTCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
 DB 1 GAGCTCACATCAGTCTCCCTCCCTCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
 QY 61 TGC CGGGAAGTCAGAGAAATTAACACCTATTTAAATTGGTATCAGCATAAACAGGGAAA 120
 DB 61 TGC CGGGAAGTCAGAGAAATTAACACCTATTTAAATTGGTATCAGCATAAACAGGGAAA 120
 QY 121 GCCCTTAAGTCTCTGATCTATGTCATCCAGTTTGCAGTGGGTGCCATCAAGGTTTC 180
 DB 121 GCCCTTAAGTCTCTGATCTATGTCATCCAGTTTGCAGTGGGTGCCATCAAGGTTTC 180
 QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
 DB 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
 QY 241 TTTGCAAGTTACTGTCAAGAGAGTCTCAGTGCCTCTGACACITTTGGCCAGGGGACC 300
 DB 241 TTTGCAAGTTACTGTCAAGAGAGTCTCAGTGCCTCTGACACITTTGGCCAGGGGACC 300
 QY 301 AAGGTGGAGATCAAAACGA 318
 DB 301 AAGGTGGAGATCAAAACGA 318

RESULT 2
 AAH68701
 ID AAH68701 standard; DNA; 321 BP.
 XX
 AC AAH68701;
 XX
 DT 14-SEP-2001 (first entry)
 XX
 DE Human anti-Rh(D) antibody clone SH13 nucleotide sequence.
 XX
 KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 red blood cell; Rh phenotype; diagnosis; therapeutic; ds.

XX Homo sapiens.
 OS
 XX US6255455-B1.
 PN
 XX 03-JUL-2001.
 PD
 XX 29-JAN-1999; 99US-00240274.
 PF
 XX 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-0088404S.
 PR 10-APR-1998; 98US-0081380P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 XX Siegel DL;
 PI
 XX WPI; 2001-388931/41.
 DR P-PSDB; AAG93644.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 PS Example 3; Col 74; 162pp; English.
 XX
 CC The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CD3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 SQ Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;

Query Match 90.4%; Score 287.6; DB 5; Length 321;
 Best Local Similarity 94.0%; Pred. No. 3.4e-81;
 Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 1 GAGCTCACATCAGTCTCCCTCCCTCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
 DB 4 GAGCTCACATCAGTCTCCCTCCCTCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 63
 QY 61 TGC CGGGAAGTCAGAGAAATTAACACCTATTTAAATTGGTATCAGCATAAACAGGGAAA 120
 DB 64 TGC CGGGAAGTCAGAGAAATTAACACCTATTTAAATTGGTATCAGCATAAACAGGGAAA 123
 QY 121 GCCCTTAAGTCTCTGATCTATGTCATCCAGTTTGCAGTGGGTGCCATCAAGGTTTC 180
 DB 124 GCCCTTAAGTCTCTGATCTATGTCATCCAGTTTGCAGTGGGTGCCATCAAGGTTTC 183
 QY 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 240
 DB 184 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTGAAGAT 243
 QY 241 TTTGCAAGTTACTGTCAAGAGAGTCTCAGTGCCTCTGACACITTTGGCCAGGGGACC 300
 DB 244 TTTGCAAGTTACTGTCAAGAGAGTCTCAGTGCCTCTGACACITTTGGCCAGGGGACC 303
 QY 301 AAGGTGGAGATCAAAACGA 318
 DB 304 AAGCTGGAGATCAAAACGA 321

RESULT 3
 ACD45365
 ID ACD45365 standard; DNA; 321 BP.
 XX

```

AC ACD45365;
XX
XX
DT 12-SEP-2003 (first entry)
XX
XX
DE Anti-Rh(D) light chain SH13 DNA.
XX
XX
KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW magnetically activated cell sorting.
XX
XX
OS Homo sapiens.
XX
XX
FN US2003040605-A1.
XX
XX
PD 27-FEB-2003.
XX
XX
PF 04-MAY-2001; 2001US-00848798.
XX
XX
PR 11-OCT-1996; 96US-0028550P.
XX
XX
PR 27-JUN-1997; 97US-00884045.
XX
XX
PR 10-APR-1998; 98US-0081380P.
XX
XX
PR 29-JAN-1999; 99US-00240274.
XX
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
XX
PI Siegel DL;
XX
XX
DR WPI; 2003-512273/48.
DR P-PSDB; ABO27451.
XX
XX
PT New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
XX
PS Claim 12; Page 57; 187pp; English.
XX
XX
CC The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents DNA encoding a human anti-Rh(D) chain
XX
XX
SQ Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;

Query Match 90.4%; Score 287.6; DB 8; Length 321;
Best Local Similarity 94.0%; Pred. No. 3.4e-81;
Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACCATCAGT 60
DB 4 GAGCTCACCAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACCATCAGT 63
QY 61 TGGCGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACCGAGGAAA 120
DB 64 TGGCGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACCGAGGAAA 123
QY 121 GCCCCTAAGTCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTT 180
DB 124 GCCCCTAAGTCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTT 183
QY 181 AGTGGCAGTGGATATGGGACAGACTTCACCTCTCAACATCAGCAGTCTGCAGCCTGAAGAT 240
DB 184 AGTGGCAGTGGATATGGGACAGACTTCACCTCTCAACATCAGCAGTCTGCAGCCTGAAGAT 243
QY 241 TTTCAGAGTTACTACTCTCAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC 300
DB 244 TTTCAGAGTTACTACTCTCAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC 303
QY 301 AAGTTGGAGATCAAAACGA 318
DB 304 AAGTTGGAGATCAAAACGA 321

RESULT 4
AAH68720

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ID AAH68720 standard; DNA; 321 BP.
XX
XX
AC AAH68720;
XX
XX
DT 14-SEP-2001 (first entry)
XX
XX
DE Human anti-Rh(D) antibody clone SH49 nucleotide sequence.
XX
XX
KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
XX
OS Homo sapiens.
XX
XX
FN US6255455-B1.
XX
XX
PD 03-JUL-2001.
XX
XX
PF 29-JAN-1999; 99US-00240274.
XX
XX
PR 11-OCT-1996; 96US-0028550P.
XX
XX
PR 27-JUN-1997; 97US-00884045.
XX
XX
PR 10-APR-1998; 98US-0081380P.
XX
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
XX
PI Siegel DL;
XX
XX
DR WPI; 2001-388931/41.
DR P-PSDB; AAG93663.
XX
XX
PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT diagnostics requiring a human instead of an animal antibody and in
PT therapeutic medicine.
XX
XX
PS Example 3; Col 79; 162pp; English.
XX
XX
CC The present invention describes an isolated Rh(D) binding protein,
CC preferably a human antibody, (I) having an amino acid sequence comprising
CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC immunostimulant activity, and can be used as an immune system stimulant.
CC (I) can be used in diagnostic and therapeutic medicines. The antibodies
CC are used in diagnostics that require human antibodies instead of animal
CC antibodies, such as determine the Rh phenotype of human red blood cells.
CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC chain CDR3 amino acid sequences which are given in the exemplification of
CC the present invention
XX
XX
SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 5; Length 321;
Best Local Similarity 92.8%; Pred. No. 3.7e-79;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGTCACTCAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACCATCAGT 60
DB 4 GAGTCACTCAGTCTCCATCTCCCTGTCGATCTGTGGAGACAGAGTCACCATCAGT 63
QY 61 TGGCGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACCGAGGAAA 120
DB 64 TGGCGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACCGAGGAAA 123
QY 121 GCCCCTAAGTCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTT 180
DB 124 GCCCCTAAGTCTCTGATCTATGCTGATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTT 183
QY 181 AGTGGCAGTGGATATGGGACAGACTTCACCTCTCAACATCAGCAGTCTGCAGCCTGAAGAT 240
DB 184 AGTGGCAGTGGATATGGGACAGACTTCACCTCTCAACATCAGCAGTCTGCAGCCTGAAGAT 243
QY 241 TTTCAGAGTTACTACTCTCAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC 300
DB 244 TTTCAGAGTTACTACTCTCAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC 303

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QY 301 AAGTGGAGATCAACGA 318
 DB 304 AAGTGGAAATCAACGA 321

RESULT 5

ID AAH68654 standard; DNA; 321 BP.
 AC AAH68654;
 XX

DT 14-SEP-2001 (first entry)
 XX

DE Human anti-Rh(D) chain I09 nucleotide sequence.
 XX

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
 XX

OS Homo sapiens.
 XX

PN US255455-B1.
 XX

PD 03-JUL-2001.
 XX

PF 29-JAN-1999; 99US-00240274.
 XX

PR 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX

PA (UYPE-) UNIV PENNSYLVANIA.
 XX

PI Siegel DL;
 XX

DR WPI; 2001-388931/41.
 DR P-PSDB; AAG93597.
 XX

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 diagnostics requiring a human instead of an animal antibody and in
 therapeutic medicine.
 PT

PS Example 2; Col 56; 162pp; English.
 XX

CC The present invention describes an isolated Rh(D) binding protein,
 preferably a human antibody, (I) having an amino acid sequence comprising
 one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 are used in diagnostics that require human antibodies instead of animal
 antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 chain CDR3 amino acid sequences which are given in the exemplification of
 the present invention
 CC

XX Sequence 321 BP; 85 A; 87 C; 73 G; 76 T; 0 U; 0 Other;
 SQ

Query Match 88.4%; Score 281.2; DB 5; Length 321;
 Best Local Similarity 92.8%; Pred. No. 3.7e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCAGTCAGTCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCACCATCACT 60
 DB 4 GAGCTCAGTCAGTCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCACCATCACT 63

QY 61 TGC CGGCGGCAAGTCAGAAATTAACACCTATTAAATGGTATCAGCATAAACAGGAAA 120

DB 64 TGC CGGCGGCAAGTCAGAGCATTAGCAGCTATTTAAATTTGTTATCAGCAGAAACAGGAAA 123

QY 121 GCGCCCTAAGCTCCTGATCTATGTCGATCCAGTTTGCAGAGTGGGGTCCCATCAAGTTTC 180

DB 124 GCGCCCTAAGCTCCTGATCTATGTCGATCCAGTTTGCAGAGTGGGGTCCCATCAAGTTTC 183

QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 240
 DB 184 AGTGCAGTGGATCTGGGACAGATTCCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 243
 QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCAGGGGACC 300
 DB 244 TTTGCAACTTATTACTGTCAACAGCTTAATAGTTACCCGTACACTTTTGGCAGGGGACC 303
 QY 301 AAGTGGAGATCAACGA 318
 DB 304 AAGTGGAGATCAACGA 321

RESULT 6

AAH68647

ID AAH68647 standard; DNA; 321 BP.
 XX

AC AAH68647;
 XX

DT 14-SEP-2001 (first entry)
 XX

DE Human anti-Rh(D) chain I02 nucleotide sequence.
 XX

KW Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
 KW

OS Homo sapiens.
 XX

PN US255455-B1.
 XX

PD 03-JUL-2001.
 XX

PF 29-JAN-1999; 99US-00240274.
 XX

PR 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX

PA (UYPE-) UNIV PENNSYLVANIA.
 XX

PI Siegel DL;
 XX

DR WPI; 2001-388931/41.
 DR P-PSDB; AAG93590.
 XX

PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 diagnostics requiring a human instead of an animal antibody and in
 therapeutic medicine.
 PT

PS Example 2; Col 54; 162pp; English.
 XX

CC The present invention describes an isolated Rh(D) binding protein,
 preferably a human antibody, (I) having an amino acid sequence comprising
 one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 are used in diagnostics that require human antibodies instead of animal
 antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 chain CDR3 amino acid sequences which are given in the exemplification of
 the present invention
 CC

XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
 SQ

Query Match 88.4%; Score 281.2; DB 5; Length 321;
 Best Local Similarity 92.8%; Pred. No. 3.7e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCAGTCAGTCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCACCATCACT 60

DB 4 GAGCTCAGTCAGTCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCACCATCACT 63

QY 61 TGCCGGGCAAGTCAGAGATTAAACACCTATTATTTAAATTTGGTATCAGATATACACGGGAAA 120
 DB 64 TGCCGGGCAAGTCAGAGATTAAACACCTATTATTTAAATTTGGTATCAGATATACACGGGAAA 123
 QY 121 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTC 180
 DB 124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTC 183
 QY 181 AGTGCCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
 DB 184 AGTGCCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 243
 QY 241 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300
 DB 244 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 303
 QY 301 AAGGTGGAGATCAAAACGA 318
 DB 304 AAGGTGGAAATCAAAACGA 321

RESULT 7

ACD45311
 ID ACD45311 standard; DNA; 321 BP.

XX AC ACD45311;

DT 12-SEP-2003 (first entry)

XX DE Anti-Rh(D) chain I02 DNA.

XX KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 XX KW magnetically activated cell sorting.

XX OS Homo sapiens.

XX PN US2003040605-A1.

XX PD 27-FEB-2003.

XX PF 04-MAY-2001; 2001US-00848798.

XX PR 11-OCT-1996; 96US-0028550P.

XX PR 27-JUN-1997; 97US-00884045.

XX PR 10-APR-1998; 98US-0081380P.

XX PR 29-JAN-1999; 99US-00240274.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX DR WPI; 2003-512273/48.

XX DR P-PSDB; ABO27397.

XX PT New human Rh(D)-binding protein useful for various diagnostic and
 XX PT therapeutic applications, including typing of blood or blood products.
 XX PS Claim 12; Page 39; 187pp; English.

XX CC The invention relates to an isolated Rh(D) binding protein. The protein
 XX CC can be used for magnetically activated cell sorting. The protein is
 XX CC useful in various diagnostic and therapeutic applications in humans,
 XX CC including typing of blood or blood products. The present sequence
 XX CC represents DNA encoding a human anti-Rh(D) chain

XX SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 8; Length 321;
 Best Local Similarity 92.8%; Pred. No. 3.7e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 1 GAGTCACTCAGTCTCCATCTCCTGCTGTCATCTGTGGGAGACAGAGTCAACCATCAGT 60

DB 4 GAGTCACTCCAGTCTCCATCTCCTGCTGTCATCTGTAGGAGACAGAGTCAACATCACT 63
 QY 61 TGCCGGGCAAGTCAGAGATTAAACACCTATTATTTAAATTTGGTATCAGATATACACGGGAAA 120
 DB 64 TGCCGGGCAAGTCAGAGATTAAACACCTATTATTTAAATTTGGTATCAGATATACACGGGAAA 123
 QY 121 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTC 180
 DB 124 GCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTTC 183
 QY 181 AGTGCCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
 DB 184 AGTGCCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 243
 QY 241 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 300
 DB 244 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTGCCTGTACACTTTTGGCCAGGGGACC 303
 QY 301 AAGGTGGAGATCAAAACGA 318
 DB 304 AAGGTGGAAATCAAAACGA 321

RESULT 8

ACD45318

ID ACD45318 standard; DNA; 321 BP.

XX AC ACD45318;

DT 12-SEP-2003 (first entry)

XX DE Anti-Rh(D) chain I09 DNA.

XX KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 XX KW magnetically activated cell sorting.

XX OS Homo sapiens.

XX PN US2003040605-A1.

XX PD 27-FEB-2003.

XX PF 04-MAY-2001; 2001US-00848798.

XX PR 11-OCT-1996; 96US-0028550P.

XX PR 27-JUN-1997; 97US-00884045.

XX PR 10-APR-1998; 98US-0081380P.

XX PR 29-JAN-1999; 99US-00240274.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX DR WPI; 2003-512273/48.

XX DR P-PSDB; ABO27404.

XX PT New human Rh(D)-binding protein useful for various diagnostic and
 XX PT therapeutic applications, including typing of blood or blood products.
 XX PS Claim 12; Page 41; 187pp; English.

XX CC The invention relates to an isolated Rh(D) binding protein. The protein
 XX CC can be used for magnetically activated cell sorting. The protein is
 XX CC useful in various diagnostic and therapeutic applications in humans,
 XX CC including typing of blood or blood products. The present sequence
 XX CC represents DNA encoding a human anti-Rh(D) chain

XX SQ Sequence 321 BP; 85 A; 87 C; 73 G; 76 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 8; Length 321;
 Best Local Similarity 92.8%; Pred. No. 3.7e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 1 GAGTCACTCAGTCTCCATCTCCTGCTGTCATCTGTGGGAGACAGAGTCAACCATCAGT 60

QY 1 GAGCTCACTCAGTCTCCATCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
 DB 4 GAGCTCACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCACT 63
 QY 61 TCCCGGGCAAGTCAGAGAAATTAACACCTATTTAAATTTGGTATCAGCATAAACCCAGGAAA 120
 DB 64 TCCCGGGCAAGTCAGAGAAATTAACACCTATTTAAATTTGGTATCAGCATAAACCCAGGAAA 123
 QY 121 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTATTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
 DB 124 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTATTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183
 QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGCTGCGAGCTGAAGAT 240
 DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGCTGCGAGCTGAAGAT 243
 QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC 300
 DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC 303
 QY 301 AAGGTGGAGATCAAAACGA 318
 DB 304 AAGGTGGAGATCAAAACGA 321

RESULT 9

ACD45384
 ID ACD45384 standard; DNA; 321 BP.

XX AC ACD45384;
 XX AC ACD45384;

DT 12-SEP-2003 (first entry)

XX DE Anti-Rh(D) light chain SH49 DNA.

XX KW Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 KW magnetically activated cell sorting.

XX OS Homo sapiens.

XX PN US2003040605-A1.

XX PD 27-FEB-2003.

XX PF 04-MAY-2001; 2001US-00848798.

XX PR 11-OCT-1996; 96US-0028550P.

XX PR 27-JUN-1997; 97US-00884045.

XX PR 10-APR-1998; 98US-0081380P.

XX PR 29-JAN-1999; 99US-00240274.

XX PA (TYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX DR WPI; 2003-512273/48.

XX DR P-PSDB; ABO27470.

XX PT New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.

XX PS Claim 12; Page 61; 187pp; English.

XX CC The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents DNA encoding a human anti-Rh(D) chain

XX SQ Sequence 321 BP; 85 A; 87 C; 77 G; 72 T; 0 U; 0 Other;

Query Match 88.4%; Score 281.2; DB 8; Length 321;

Best Local Similarity 92.8%; Pred. No. 3.7e-79;
 Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCTCCATCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCACT 60
 DB 4 GAGCTCACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCACT 63
 QY 61 TCCCGGGCAAGTCAGAGAAATTAACACCTATTTAAATTTGGTATCAGCATAAACCCAGGAAA 120
 DB 64 TCCCGGGCAAGTCAGAGAAATTAACACCTATTTAAATTTGGTATCAGCATAAACCCAGGAAA 123
 QY 121 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTATTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
 DB 124 GCCCTTAAGCTCCTGATCTATGCTGATCCAGTATTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183
 QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGCTGCGAGCTGAAGAT 240
 DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGCTGCGAGCTGAAGAT 243
 QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC 300
 DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACC 303
 QY 301 AAGGTGGAGATCAAAACGA 318
 DB 304 AAGGTGGAGATCAAAACGA 321

RESULT 10

AAT66781

ID AAT66781 standard; cDNA; 321 BP.

XX AC AAT66781;

DT 29-JAN-1998 (first entry)

XX DE Anti-cancer specific antigen MAb light chain variable region cDNA.

XX KW Light chain; variable region; cancer specific antigen; human;
 KW monoclonal antibody; hMAb; diagnosis; cancer; immunotherapy;
 KW purification; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT mat_peptide 1..321

XX FT /*tag= a

XX PN JP09098786-A.

XX PD 15-APR-1997.

XX PF 06-OCT-1995; 95JP-00284400.

XX PR 06-OCT-1995; 95JP-00284400.

XX PA (MOMI) MORINAGA & CO LTD.

XX PA (SHKJ) SHINGIJUTSU JIGYODAN.

XX DR WPI; 1997-275445/25.

XX DR P-PSDB; AAW16649.

XX PT cDNA encoding human monoclonal antibody - useful in medicine, or to
 PT purify cancer specific antigen.

XX PS Claim 2; Fig 2; 7pp; Japanese.

XX CC The present sequence encodes the light chain variable region of an anti-
 CC cancer specific antigen human monoclonal antibody (hMAb). The hMAb can be
 CC used in medicine, e.g. clinical diagnosis of cancer or immunotherapy, or
 CC to purify cancer specific antigen. The industrial scale production of
 CC large amounts of the hMAb is made feasible by genetic engineering using
 CC the hMAb cDNA

PT diagnostics requiring a human instead of an animal antibody and in
 XX therapeutic medicine.
 XX Siegel DL;
 PS Example 2; Col 57; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 SQ Sequence 321 BP; 82 A; 88 C; 77 G; 74 T; 0 U; 0 Other;
 Query Match 87.9%; Score 279.6; DB 5; Length 321;
 Best Local Similarity 92.5%; Pred. No. 1.2e-78;
 Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 GAGCTCACTCAGTCTCCATCTCCCTGCTGCTGATCTGGGAGACAGAGTCAACATCACT 60
 DB |||||
 QY 4 GAGCTCACCCAGTCTCCATCTCCCTGCTGCTGATCTGGGAGACAGAGTCAACATCACT 63
 DB |||||
 QY 61 TCCCGGGCAAGTCAGAGATTAAACACCTATTATAATTGGTATCAGCATAAACCCAGGAAA 120
 DB |||||
 QY 64 TCCCGGGCAAGTCAGAGATTAAACACCTATTATAATTGGTATCAGCATAAACCCAGGAAA 123
 DB |||||
 QY 121 GCCCTTAAGTCTCTGATCTATGCTGATCTCCATCTCCCTGCTGCTGATCTGGGAGACAGAGTCAACATCACT 180
 DB |||||
 QY 124 GCCCTTAAGTCTCTGATCTATGCTGATCTCCATCTCCCTGCTGCTGATCTGGGAGACAGAGTCAACATCACT 183
 DB |||||
 QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACATCAGCAGTCTGAGCCTGAAGAT 240
 DB |||||
 QY 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACATCAGCAGTCTGAGCCTGAAGAT 243
 DB |||||
 QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTGCTGATCACTTTTGGCCAGGGACC 300
 DB |||||
 QY 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTGCTGATCACTTTTGGCCAGGGACC 303
 DB |||||
 QY 301 AAGGTGGAGATCAAAACGA 318
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 DB |||||
 RESULT 13
 AAH68724
 ID AAH68724 standard; DNA; 321 BP.
 AC AAH68724;
 XX
 XX 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) antibody clone SH54 nucleotide sequence.
 DE
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
 XX
 XX Homo sapiens.
 OS
 XX US6255455-B1.
 PN
 XX
 XX 03-JUL-2001.
 PD
 XX 29-JAN-1999; 99US-00240274.
 PF
 XX 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX

(UYPE-) UNIV PENNSYLVANIA.
 XX Siegel DL;
 XX WPI; 2001-389331/41.
 DR P-PSDB; AAG93667.
 XX
 PT New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 PS Example 3; Col 80; 162pp; English.
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 SQ Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;
 Query Match 87.9%; Score 279.6; DB 5; Length 321;
 Best Local Similarity 92.5%; Pred. No. 1.2e-78;
 Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 GAGCTCACTCAGTCTCCATCTCCCTGCTGCTGATCTGGGAGACAGAGTCAACATCACT 60
 DB |||||
 QY 4 GAGCTCACCCAGTCTCCATCTCCCTGCTGCTGATCTGGGAGACAGAGTCAACATCACT 63
 DB |||||
 QY 61 TCCCGGGCAAGTCAGAGATTAAACACCTATTATAATTGGTATCAGCATAAACCCAGGAAA 120
 DB |||||
 QY 64 TCCCGGGCAAGTCAGAGATTAAACACCTATTATAATTGGTATCAGCATAAACCCAGGAAA 123
 DB |||||
 QY 121 GCCCTTAAGTCTCTGATCTATGCTGATCTCCATCTCCCTGCTGCTGATCTGGGAGACAGAGTCAACATCACT 180
 DB |||||
 QY 124 GCCCTTAAGTCTCTGATCTATGCTGATCTCCATCTCCCTGCTGCTGATCTGGGAGACAGAGTCAACATCACT 183
 DB |||||
 QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCACATCAGCAGTCTGAGCCTGAAGAT 240
 DB |||||
 QY 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCACATCAGCAGTCTGAGCCTGAAGAT 243
 DB |||||
 QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGGCTGCTGATCACTTTTGGCCAGGGACC 300
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 DB |||||
 QY 301 AAGGTGGAGATCAAAACGA 318
 DB |||||
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 DB |||||
 RESULT 14
 AAH68652
 ID AAH68652 standard; DNA; 321 BP.
 XX
 AC AAH68652;
 XX
 XX 14-SEP-2001 (first entry)
 DE Human anti-Rh(D) chain I07 nucleotide sequence.
 DE
 DE Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KW red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
 XX
 XX Homo sapiens.
 OS
 XX US6255455-B1.
 PN
 XX

PD 03-JUL-2001.
 XX
 XX 29-JAN-1999; 99US-00240274.
 XX
 XX 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX Siegel DL;
 PI
 XX WPI; 2001-388931/41.
 DR P-PSDB; AAG93595.
 XX
 XX New isolated protein, preferably a human anti-Rh(D) antibody for use in
 PT diagnostics requiring a human instead of an animal antibody and in
 PT therapeutic medicine.
 XX
 XX Example 2; Col 55; 162pp; English.
 PS
 XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93558 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.
 CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.
 CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention
 XX
 XX Sequence 321 BP; 85 A; 87 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 87.9%; Score 279.6; DB 5; Length 321;
 Best Local Similarity 92.5%; Pred. No. 1.2e-78;
 Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 GAGTCACTCAGTCTCCATCTCTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 60
 Db 4 GAGTCACTCAGTCTCCATCTCTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 63
 QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATTAACACCGGAAA 120
 Db 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATTAACACCGGAAA 123
 QY 121 GCCCCTAAGCTCCTGATCTATGTCGATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 180
 Db 124 GCCCCTAAGCTCCTGATCTATGTCGATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 183
 QY 181 AGTGGCAGTGGATATGGGACAGACTTCACCTCACCATCAGCAGTCTGACGCTGAAGAT 240
 Db 184 AGTGGCAGTGGATATGGGACAGACTTCACCTCACCATCAGCAGTCTGACGCTGAAGAT 243
 QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGGACC 300
 Db 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGGACC 303
 QY 301 AAGGTGGAGATCAACGA 318
 Db 304 AAGGTGGAGATCAACGA 321

RESULT 15
 ACD45388
 ID ACD45388 standard; DNA; 321 BP.
 XX
 AC ACD45388;
 XX
 DT 12-SEP-2003 (first entry)
 XX
 DE Anti-Rh(D) light chain SH54 DNA.

XX Human; ds; gene; RH(D) binding protein; blood typing; blood product;
 KW magnetically activated cell sorting.
 XX
 XX Homo sapiens.
 XX
 XX US2003040605-A1.
 XX
 XX 27-FEB-2003.
 XX
 XX 04-MAY-2001; 2001US-00848798.
 XX
 XX 11-OCT-1996; 96US-0028550P.
 PR 27-JUN-1997; 97US-00884045.
 PR 10-APR-1998; 98US-0081380P.
 PR 29-JAN-1999; 99US-00240274.
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX Siegel DL;
 PI
 XX WPI; 2003-512273/48.
 DR P-PSDB; ABO27474.
 XX
 XX New human Rh(D) binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.
 XX
 XX Claim 12; Page 61; 187pp; English.
 PS
 XX The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents DNA encoding a human anti-Rh(D) chain
 XX
 XX Sequence 321 BP; 86 A; 86 C; 76 G; 73 T; 0 U; 0 Other;

Query Match 87.9%; Score 279.6; DB 8; Length 321;
 Best Local Similarity 92.5%; Pred. No. 1.2e-78;
 Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 QY 1 GAGTCACTCAGTCTCCATCTCTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 60
 Db 4 GAGTCACTCAGTCTCCATCTCTCTGTCATCTGTGGGAGACAGAGTCACCATCAGT 63
 QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATTAACACCGGAAA 120
 Db 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATTAACACCGGAAA 123
 QY 121 GCCCCTAAGCTCCTGATCTATGTCGATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 180
 Db 124 GCCCCTAAGCTCCTGATCTATGTCGATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTT 183
 QY 181 AGTGGCAGTGGATATGGGACAGACTTCACCTCACCATCAGCAGTCTGACGCTGAAGAT 240
 Db 184 AGTGGCAGTGGATATGGGACAGACTTCACCTCACCATCAGCAGTCTGACGCTGAAGAT 243
 QY 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGGACC 300
 Db 244 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTCCCTGCTACACTTTTGGCCAGGGGACC 303
 QY 301 AAGGTGGAGATCAACGA 318
 Db 304 AAGGTGGAGATCAACGA 321

Search completed: August 13, 2004, 01:35:52
 Job time : 209.182 secs

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 03:58:10 ; Search time 706.827 Seconds
(without alignments)
2207.472 Million cell updates/sec

Title: US-10-027-725A-4

Perfect score: 318

Sequence: 1 gagctcactcagctccatc.....ccaaagtggagatcaaacga 318

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
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- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	318	15	US-10-027-725A-4
2	287.6	90.4	321	10	US-09-848-798-199
3	281.2	88.4	321	10	US-09-848-798-102
4	281.2	88.4	321	10	US-09-848-798-109
5	281.2	88.4	321	10	US-09-848-798-218
6	279.6	87.9	321	10	US-09-848-798-107
7	279.6	87.9	321	10	US-09-848-798-113
8	279.6	87.9	321	10	US-09-848-798-221
9	279.6	87.9	321	10	US-09-848-798-222
10	277.6	87.3	324	17	US-10-344-514-3
11	277.6	87.3	324	17	US-10-344-514-4
12	277.6	87.3	333	15	US-10-203-754A-60
13	277.6	87.3	900	15	US-10-203-754A-64
14	276.4	86.9	321	10	US-09-848-798-201

15	276.4	86.9	321	10	US-09-848-798-211	Sequence 211, App
16	276.2	86.9	324	10	US-09-848-798-101	Sequence 101, App
17	276.2	86.9	324	10	US-09-848-798-112	Sequence 112, App
18	276.2	86.9	324	10	US-09-848-798-210	Sequence 210, App
19	276	86.8	720	9	US-09-192-854-1	Sequence 1, Appli
20	276	86.8	720	9	US-09-968-561A-1	Sequence 1, Appli
21	276	86.8	720	10	US-09-968-744A-1	Sequence 1, Appli
22	276	86.8	720	13	US-09-968-561A-1	Sequence 1, Appli
23	275.4	86.6	729	15	US-10-216-484-125	Sequence 125, App
24	275.4	86.6	729	15	US-10-384-933-125	Sequence 125, App
25	274.8	86.4	321	10	US-09-848-798-105	Sequence 105, App
26	274.8	86.4	321	10	US-09-848-798-216	Sequence 216, App
27	274.2	86.2	322	17	US-10-038-591-54	Sequence 54, Appl
28	273.8	86.1	333	15	US-10-203-754A-61	Sequence 61, Appl
29	273.8	86.1	900	15	US-10-203-754A-65	Sequence 65, Appl
30	273.2	85.9	321	10	US-09-848-798-104	Sequence 104, App
31	273.2	85.9	321	10	US-09-848-798-106	Sequence 106, App
32	273.2	85.9	321	10	US-09-848-798-215	Sequence 215, App
33	273.2	85.9	321	10	US-09-848-798-217	Sequence 217, App
34	273	85.8	324	10	US-09-848-798-206	Sequence 206, App
35	271.8	85.5	322	16	US-10-309-762-226	Sequence 226, App
36	271.8	85.5	322	16	US-10-309-762-227	Sequence 227, App
37	271.4	85.3	324	10	US-09-848-798-110	Sequence 110, App
38	270.6	85.1	714	15	US-10-153-382-18	Sequence 18, Appl
39	270.6	85.1	1106	16	US-10-264-049-121	Sequence 121, App
40	270.2	85.0	322	16	US-10-309-762-233	Sequence 233, App
41	270.2	85.0	322	16	US-10-309-762-233	Sequence 233, App
42	270	84.9	321	10	US-09-848-798-205	Sequence 205, App
43	270	84.9	321	10	US-09-848-798-207	Sequence 207, App
44	269.6	84.8	324	17	US-10-344-514-7	Sequence 7, Appli
45	269.6	84.8	324	17	US-10-344-514-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-027-725A-4
; Sequence 4, Application US/10027725A
; Publication No. US20030082659A1
; GENERAL INFORMATION:
; APPLICANT: Flicker, Sabine
; TITLE OF INVENTION: Group 2 Allergen Specific IgE-fabs and Use Thereof
; FILE REFERENCE: 25401-4
; CURRENT APPLICATION NUMBER: US/10/027,725A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/259,436
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-027-725A-4

Query Match 100.0%; Score 318; DB 15; Length 318;
Best Local Similarity 100.0%; Pred. No. 4, 1e-97;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GAGCTCAGTCTCCATCCCTCCCTGCTGATCTGTGGGAGACAGATCACCATCAGT	60
Db	1	GAGCTCAGTCTCCATCCCTCCCTGCTGATCTGTGGGAGACAGATCACCATCAGT	60
QY	61	TCCGGGCAAGTCAGAGATTAACTATTAAATTTGATCAGCATAAACCGGAAA	120
Db	61	TCCGGGCAAGTCAGAGATTAACTATTAAATTTGATCAGCATAAACCGGAAA	120
QY	121	GCCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAGAGTGGGTCCCATCAAGTTTC	180
Db	121	GCCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAGAGTGGGTCCCATCAAGTTTC	180
QY	181	AGTGGCAGTGGATATGGGACAGACTTCTACTCCATCCATCAGCAGTCTGCAGCCTGAAGAT	240

Db 181 AGTGGCAGTGGATGAGCAGACTTCACCTCCACATCAGCATCTGCAGCCTGAAGAT 240
QY 241 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGACC 300
Db 241 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGACC 300
QY 301 AAGGTGGAGATCAACGA 318
Db 301 AAGGTGGAGATCAACGA 318

RESULT 2

US-09-848-798-199
; Sequence 199, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-199

Query Match 90.4%; Score 287.6; DB 10; Length 321;
Best Local Similarity 94.0%; Pred. No. 8.2e-87; Indels 0; Gaps 0;
Matches 299; Conservative 0; Mismatches 19

QY 1 GAGTCTCACTAGTCTCCATCCTCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCTCACTAGTCTCCATCCTCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
QY 61 TCCCGGGCAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCGGAAA 120
Db 64 TCCCGGGCAGTCAGAGCAATTAGCAGCTATTAAATTTGGTATCAGCATAAACCGGAAA 123
QY 121 GCCCCTAAGCTCTGATCTATGTCGATCCATCTGTCATCTGTGGAGACAGAGTCACCATCAGTTC 180
Db 124 GCCCCTAAGCTCTGATCTATGTCGATCCATCTGTCATCTGTGGAGACAGAGTCACCATCAGTTC 183
QY 181 AGTGCAGTGGATATGGACAGACTTCACTCTCACCACAGAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGCAGTGGATCTGGACAGATTTCACTCTCACCACAGAGTCTGCAGCCTGAAGAT 243
QY 241 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGACC 300
Db 244 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGACC 303
QY 301 AAGGTGGAGATCAACGA 318
Db 304 AAGGTGGAGATCAACGA 321

RESULT 3

US-09-848-798-102
; Sequence 102, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 102
US-09-848-798-102

Query Match 88.4%; Score 281.2; DB 10; Length 321;
Best Local Similarity 92.8%; Pred. No. 1.2e-84;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 GAGTCTCACTAGTCTCCATCCTCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCTCACTAGTCTCCATCCTCCTGCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
QY 61 TCCCGGGCAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCGGAAA 120
Db 64 TCCCGGGCAGTCAGAGCAATTAGCAGCTATTAAATTTGGTATCAGCATAAACCGGAAA 123
QY 121 GCCCCTAAGCTCTGATCTATGTCGATCCATCTGTCATCTGTGGAGTTCCTCAAGGTTTC 180
Db 124 GCCCCTAAGCTCTGATCTATGTCGATCCATCTGTCATCTGTGGAGTTCCTCAAGGTTTC 183
QY 181 AGTGCAGTGGATATGGACAGACTTCACTCTCACCACAGAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGCAGTGGATCTGGACAGATTTCACTCTCACCACAGAGTCTGCAGCCTGAAGAT 243
QY 241 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGACC 300
Db 244 TTTCGAAGTACTACTGTCAGAGAGTCTCAGTCCCTCGTACACTTTTGCCAGGGACC 303
QY 301 AAGGTGGAGATCAACGA 318
Db 304 AAGGTGGAGATCAACGA 321

RESULT 4

US-09-848-798-109
; Sequence 109, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 109
US-09-848-798-109

Query Match 88.4%; Score 281.2; DB 10; Length 321;

Best Local Similarity 92.8%; Pred. No. 1.2e-84;	
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;	
Qy 1	GAGCTCACTCAGTCTCCATCTCCCTGTCGTGCATCTGTGGGACAGAGTCACCATCAGT 60
Db	
4	GAGCTCACCCAGTCTCCATCTCCCTGTCGTCACTGTGTAGGACAGAGTCACCATCACT 63
Qy 61	TGCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCGGGAAA 120
Db	
64	TGCCGGGCAAGTCAGAGCAITTAGCAGCTATTAAATTTGTTATCAGCAGAAAACCGGGAAA 123
Qy 121	GCCCTTAAGCTCCTGATCTATGCTGTCATCCAGTTTGCAAAGTGGGTCCTCATCAAGGTTTC 180
Db	
124	GCCCTTAAGCTCCTGATCTATGCTGTCATCCAGTTTGCAAAGTGGGTCCTCATCAAGGTTTC 183
Qy 181	AGTGGCAGTGGATATGGGACAGATTCCTCACTCTCACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db	
184	AGTGGCAGTGGATCTGGGACAGATTCCTCACTCTCACCATCAGCAGTCTGCACACCTGAAGAT 243
Qy 241	TTTTCAAAGTTACTACTGTCAAAGAGAGTCTCAGTCGCTCGTACACTTTTGGCCAGGGGACC 300
Db	
244	TTTTCGACTTATTACTGTCAACAGCTTAATAGTTACCGGTACACTTTTGGCCAGGGGACC 303
Qy 301	AAGGTGGAGATCAAACGA 318
Db	
304	AAGCTGGAGATCAAACGA 321

RESULT 5
US-09-848-798-218
US-09-848-798-218, Application US/09848798
; Sequence 218, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-848-798-218

```

Qy      241  TTTGCAAGTTACTACTGTCAGAGAGTCTCAAGTGCCTCGTACACACTTTTGGCCAGGGGACC 300
Db      244  TTTGCAACTTACTACTGTGTCACACAGAGTTACAGTACCCCGTGGACGTTGGCCAAAGGACC 303
Qy      301  AAGGTGGAGATCAAAACGA 318
Db      304  AAGGTGGAAATCAAAACGA 321

RESULT 6
US-09-848-798-107
; Sequence 107, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I07
US-09-848-798-107

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RESULT 7
US-09-848-798-113
; Sequence 113, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798

; CURRENT FILING DATE: 2001-05-04	
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274	
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29	
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550	
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11	
; NUMBER OF SEQ ID NOS: 224	
; SOFTWARE: PatentIn Ver. 2.0	
; SEQ ID NO 113	
; LENGTH: 321	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
; FEATURE:	
; OTHER INFORMATION: anti-Rh(D) chain I13	
US-09-848-798-113	
Query Match 87.9%; Score 279.6; DB 10; Length 321;	
Best Local Similarity 92.5%; Pred. No. 4.2e-84;	
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;	
Qy	1 GAGCTCACTCAGTCTCCATCCTCCTGCTGATCTGCTGAGAGAGAGAGTCAACATCACT 60
Db	4 GAGCTCACTCAGTCTCCATCCTCCTGCTGATCTGCTGAGAGAGAGTCAACATCACT 63
Qy	61 TCCCGGCAAGTCAGAGAAATAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 120
Db	64 TCCCGGCAAGTCAGAGAAATAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 123
Qy	121 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
Db	124 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183
Qy	181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCCACATCAGCATCTGCAGCCTGAAGAT 240
Db	184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCCACATCAGCATCTGCAGCCTGAAGAT 243
Qy	241 TTTGCAAGTTACTACTCTCAAGAGAGTCTCAGTCGCTCGTACACTTTTGGCCAGGGACC 300
Db	244 TTTGCAAGTTACTACTCTCAAGAGAGTCTCAGTCGCTCGTACACTTTTGGCCAGGGACC 303
Qy	301 AAGGTGGAGATCAAAACGA 318
Db	304 AAGGTGGAGATCAAAACGA 321
RESULT 9	
US-09-848-798-222	
; Sequence 222, Application US/09848798	
; Publication No. US20030040605A1	
; GENERAL INFORMATION:	
; APPLICANT: Siegel, Donald L.	
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL	
; FILE REFERENCE: 09596-42U2	
; CURRENT APPLICATION NUMBER: US/09/848,798	
; PRIOR FILING DATE: 2001-05-04	
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274	
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29	
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550	
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11	
; NUMBER OF SEQ ID NOS: 224	
; SOFTWARE: PatentIn Ver. 2.0	
; SEQ ID NO 222	
; LENGTH: 321	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
; FEATURE:	
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54	
US-09-848-798-222	
Query Match 87.9%; Score 279.6; DB 10; Length 321;	
Best Local Similarity 92.5%; Pred. No. 4.2e-84;	
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;	
Qy	1 GAGCTCACTCAGTCTCCATCCTCCTGCTGATCTGCTGAGAGAGAGTCAACATCACT 60
Db	4 GAGCTCACTCAGTCTCCATCCTCCTGCTGATCTGCTGAGAGAGAGTCAACATCACT 63
Qy	61 TCCCGGCAAGTCAGAGAAATAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 120
Db	64 TCCCGGCAAGTCAGAGAAATAACACCTATTAAATTTGGTATCAGCATAAACCCAGGAAA 123
Qy	121 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 180
Db	124 GCCCTTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTTC 183
Qy	181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCCACATCAGCATCTGCAGCCTGAAGAT 240
Db	184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCCACATCAGCATCTGCAGCCTGAAGAT 243
Qy	241 TTTGCAAGTTACTACTCTCAAGAGAGTCTCAGTCGCTCGTACACTTTTGGCCAGGGACC 300
Db	244 TTTGCAAGTTACTACTCTCAAGAGAGTCTCAGTCGCTCGTACACTTTTGGCCAGGGACC 303
Qy	301 AAGGTGGAGATCAAAACGA 318
Db	304 AAGGTGGAGATCAAAACGA 321
RESULT 8	
US-09-848-798-221	
; Sequence 221, Application US/09848798	
; Publication No. US20030040605A1	
; GENERAL INFORMATION:	
; APPLICANT: Siegel, Donald L.	
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL	
; FILE REFERENCE: 09596-42U2	
; CURRENT APPLICATION NUMBER: US/09/848,798	
; PRIOR FILING DATE: 2001-05-04	
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274	
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29	
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550	
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11	
; NUMBER OF SEQ ID NOS: 224	
; SOFTWARE: PatentIn Ver. 2.0	
; SEQ ID NO 221	
; LENGTH: 321	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
; FEATURE:	
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52	
US-09-848-798-221	
Query Match 87.9%; Score 279.6; DB 10; Length 321;	
Best Local Similarity 92.5%; Pred. No. 4.2e-84;	
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;	

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QY 301 AAGTGGAGATCAAAACGA 318
Db 304 AAGTGGAAATCAAAACGA 321

RESULT 10
US-10-344-514-3
; Sequence 3, Application US/10344514
; Publication No. US20040120951A1
; GENERAL INFORMATION:
; APPLICANT: NAKASHIMA, Toshihiro et al.
; TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
; FILE REFERENCE: 0020-5111P
; CURRENT APPLICATION NUMBER: US/10/344,514
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP 2001-177640
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-344-514-3

Query Match      87.3%; Score 277.6; DB 17; Length 324;
Best Local Similarity 92.4%; Pred. No. 2e-83;
Matches 292; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 2 AGCTCACTCAGTCTCCATCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCAGTT 61
Db 8 AGTTGACCCAGTCTCCATCCCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCATT 67

QY 62 GCCGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGGAAG 121
Db 68 GCCGGCAAGTCAGAGCAATTAGCAGCTATTAAATTTGGTATCAGCAGAAACCCAGGGAAG 127

QY 122 CCCCTAAGCTCCTGATCTATGCTGATCCAGCTTTGCAAGTGGGTCCCATCAAGGTTCA 181
Db 128 CCCCTAAGCTCCTGATCTATGCTGATCCAGCTTTGCAAGTGGGTCCCATCAAGGTTCA 187

QY 182 GTGGCAGTGGATATGGGACAGACTTCACTCTCAACATCAGCAGTCTGCAGCTTGAAGATT 241
Db 188 GTGGCAGTGGATCTGGGACAGATTTCATCTCAGCATCAGCAGTCTGCAACCTGAAAGATT 247

QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGGACCA 301
Db 248 TTGCAACTTACTACTGTCAAGAGATTACAGTACCCCGCTCACTTTGGCGGGAGGACCA 307

QY 302 AGGTGGAGATCAAAACG 317
Db 308 AGGTGGAGATCAAAACG 323

RESULT 11
US-10-203-754A-60
; Sequence 60, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSUURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 60
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-754A-60

Query Match      87.3%; Score 277.6; DB 15; Length 333;
Best Local Similarity 92.4%; Pred. No. 2e-83;
Matches 292; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 2 AGTCTACTCAGTCTCCATCCCTCCCTGCTGTCATCTGTGGGAGACAGAGTCACCATCAGTT 61
Db 8 AGATGACCCAGTCTCCATCCCTCCCTGCTGTCATCTGTAGGAGACAGAGTCACCATCACTI 67

QY 62 GCCGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATAAACCCAGGGAAG 121
Db 68 GCCGGCAAGTCAGAGCAATTAGCAGCTATTAAATTTGGTATCAGCAGAAACCCAGGGAAG 127

QY 122 CCCCTAAGCTCCTGATCTATGCTGATCCAGCTTTGCAAGTGGGTCCCATCAAGGTTCA 181
Db 128 CCCCTAAGCTCCTGATCTATGCTGATCCAGCTTTGCAAGTGGGTCCCATCAAGGTTCA 187
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QY 182 GTGCAGTGGATATGGGACAGATTCCTCTCACCATCAGCAGTCTGCAGCTGAAGATT 241
DB 188 GTGCAGTGGATCTGGGACAGATTCCTCTCACCATCAGCAGTCTGAACCTGAAGATT 247
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACCA 301
DB 248 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACCA 307
QY 302 AGGTGGAGATCAACG 317
DB 308 AGGTGGAGATCAACG 323

RESULT 13

US-10-203-754A-64
; Sequence 64, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
; APPLICANT: ITAMI, Seima
; APPLICANT: SEKI, Makoto
; APPLICANT: MATSUURA, Yoshiharu
; APPLICANT: SHIBUI, Tatsuro
; APPLICANT: YOTSUMOTO, Yoshihisa
; APPLICANT: MIYAMURA, Tatsuo
; TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
; FILE REFERENCE: P22257
; CURRENT APPLICATION NUMBER: US/10/203,754A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/JP01/00967
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-203-754A-64

Query Match 87.3%; Score 277.6; DB 15; Length 900;
Best Local Similarity 92.4%; Pred. No. 38-83;
Matches 292; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 2 AGCTCACTCAGTCTCCATCCTCCTGCTGTCATCTGTGGGACAGAGTCACCATCAGTT 61
DB 503 AGATGACCCAGTCTCCATCCTCCTGCTGTCATCTGTAGGACAGAGTCACCATCATT 562
QY 62 GCCGGGCAAGTCAGAGAAATTAACACTATTAAATGGTATCAGCATAAACAGGGAAG 121
DB 563 GCCGGGCAAGTCAGAGCAATTAACAGCTATTAAATGGTATCAGCAGAAACAGGGAAG 622
QY 122 CCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAGTGGGGTCCCATCAAGTTCA 181
DB 623 CCCCTAAGCTCTGATCTATGTCATCCAGTTTGCAGTGGGGTCCCATCAAGTTCA 682
QY 182 GTGCAGTGGATATGGGACAGATTCCTCTCACCATCAGCAGTCTGCAGCTGAAGATT 241
DB 683 GTGCAGTGGATCTGGGACAGATTCCTCTCACCATCAGCAGTCTGCAACCTGAAGATT 742
QY 242 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACCA 301
DB 743 TTGCAACTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACCA 802
QY 302 AGGTGGAGATCAACG 317
DB 803 AGGTGGAGATCAACG 818

RESULT 14

US-09-848-798-201
; Sequence 201, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.

; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-848-798-201

Query Match 86.9%; Score 276.4; DB 10; Length 321;
Best Local Similarity 91.8%; Pred. No. 5.1e-83;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 1 GAGCTCACTCAGTCTCCATCCTCCTGCTGTCATCTGTGGGACAGAGTCACCATCAGT 60
DB 4 GAGCTCACCCAGTCTCCATCCTCCTGCTGTCATCTGTAGGACAGAGTCACCATCAGT 63
QY 61 TCCGGGCAAGTCAGAGAAATTAACACTATTAAATGGTATCAGCATAAACAGGGAAA 120
DB 64 TCCGGGCAAGTCAGAGCAATTAGCAGCTATTAAATGGTATCAACAGAAACAGGGAAA 123
QY 121 GCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAGTGGGGTCCCATCAAGTTTC 180
DB 124 GCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAGTGGGGTCCCATCAAGTTTC 183
QY 181 AGTGGCAGTGGATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 240
DB 184 AGTGGCAGTGGATCTGGGACAGATTCCTCTCACCATCAGCAGTCTGCAGCTCAAGAT 243
QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTAACATTTTGGCCAGGGGACC 300
DB 244 TTGCAACTTACTACTGTCAAGAGATTCACATGATCCCTCCCACTTCGGCGGAGGACC 303
QY 301 AAGGTGGAGATCAACGA 318
DB 304 AAGGTGGAGATCAACGA 321

RESULT 15

US-09-848-798-211
; Sequence 211, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-848-798-211

Query Match		86.9%;	Score 276.4;	DB 10;	Length 321;
Best Local Similarity		91.8%;	Pred. No. 5.1e-83;		
Matches 292;		Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;
Qy	1	GAGTCACTCAGTCTCCATCCCTCCCTGCTGCACTCTGTAGGAGACAGAGTCACCATCACT	60		
Db	4	GAGTCACTCAGTCTCCATCCCTCCCTGCTGCACTCTGTAGGAGACAGAGTCACCATCACT	63		
Qy	61	TGCCGGGCAAGTCAGAGATTAAACACCTATTATATTTGGTATCAGCATAAACCCAGGGAAA	120		
Db	64	TGCCGGGCAAGTCAGAGATTAGCAGCTATTATAATTTGGTATCAGCATAAACCCAGGGAAA	123		
Qy	121	GCCCTAAGCTCCTGATCTATGCTGCACTCCAGTTTGCAAGTGGGTTCCCATCAAGGTTT	180		
Db	124	TCCCTAAGCTCCTGATCTATGCTGCACTCCAGTTTGCAAGTGGGTTCCCATCAAGGTTT	183		
Qy	181	AGTGGCAGTGGATATGGGACACAGACTTCACTCTACCATCAGCAGTCTGCAACCTGAAGAT	240		
Db	184	AGTGGCAGTGGATCTGGGACACAGATTTCATCTCACCATCAGCAGTCTGCAACCTGAAGAT	243		
Qy	241	TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTGACACTTTTGGCCAGGGGACC	300		
Db	244	TTTGCACCTTACTACTGTCAACAGAGTTACAGTACCCCTCCGGCTTTTGGGCCCTGGGACC	303		
Qy	301	AAGTGGAGATCAAAACGA	318		
Db	304	AAAGTGGATATCAAAACGA	321		

Search completed: August 13, 2004, 19:18:23
Job time : 707.827 secs

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:21:37 ; Search time 44.9697 Seconds

(without alignments)

3924.296 Million cell updates/sec

Title: US-10-027-725A-4

Perfect score: 318

Sequence: 1 gagctcactcagctccatc.....ccaaagtgagatcaaacga 318

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
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5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	287.6	90.4	321	3	US-09-240-274-199
2	281.2	88.4	321	3	US-09-240-274-102
3	281.2	88.4	321	3	US-09-240-274-109
4	281.2	88.4	321	3	US-09-240-274-218
5	279.6	87.9	321	3	US-09-240-274-107
6	279.6	87.9	321	3	US-09-240-274-113
7	279.6	87.9	321	3	US-09-240-274-221
8	279.6	87.9	321	3	US-09-240-274-222
9	276.4	86.9	321	3	US-09-240-274-201
10	276.4	86.9	321	3	US-09-240-274-211
11	276.2	86.9	324	3	US-09-240-274-101
12	276.2	86.9	324	3	US-09-240-274-112
13	276.2	86.9	324	3	US-09-240-274-210
14	274.8	86.4	321	3	US-09-240-274-105
15	274.8	86.4	321	3	US-09-240-274-216
16	273.2	85.9	321	3	US-09-240-274-104
17	273.2	85.9	321	3	US-09-240-274-106
18	273.2	85.9	321	3	US-09-240-274-215
19	273.2	85.9	321	3	US-09-240-274-217
20	273	85.8	324	3	US-09-240-274-206
21	271.4	85.3	324	4	US-09-240-274-110
22	270.6	85.1	714	4	US-09-472-087-62
23	270	84.9	321	3	US-09-240-274-205
24	270	84.9	321	3	US-09-240-274-207
25	268.2	84.3	324	3	US-09-240-274-224
26	266.8	83.9	321	3	US-09-240-274-108
27	266.8	83.9	321	3	US-09-240-274-203

Sequence 103, App
Sequence 47, Appl
Sequence 48, Appl
Sequence 13, Appl
Sequence 200, App
Sequence 213, App
Sequence 23, Appl
Sequence 44, Appl
Sequence 50, Appl
Sequence 358, App
Sequence 206, App
Sequence 212, App
Sequence 49, Appl
Sequence 208, App
Sequence 114, App
Sequence 198, App
Sequence 31, Appl
Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-09-240-274-199

; Sequence 199, Application US/09240274

; Patent No. 6255455

; GENERAL INFORMATION:

; APPLICANT: Siegel, Donald L.

; TITLE OF INVENTION: Rh(D) -BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL

; FILE REFERENCE: 09596-4202

; CURRENT APPLICATION NUMBER: US/09/240,274

; CURRENT FILING DATE: 1999-01-29

; EARLIER APPLICATION NUMBER: 60/081,380

; EARLIER FILING DATE: 1998-04-10

; EARLIER APPLICATION NUMBER: 60/028,550

; EARLIER FILING DATE: 1996-10-11

; NUMBER OF SEQ ID NOS: 224

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 199

; LENGTH: 321

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: anti-Rh(D) antibody clone SH13

; US-09-240-274-199

Query Match 90.4%; Score 287.6; DB 3; Length 321;
Best Local Similarity 94.0%; Pred. No. 4e-91;
Matches 299; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy	1	GAGTCACTCAGTCTCCATCCTCCCTGTCGTCATCTGTGGGAGACAGAGTCACCATCAGT	60
Db	4	GAGTCACTCAGTCTCCATCCTCCCTGTCGTCATCTGTGGGAGACAGAGTCACCATCAGT	63
Qy	61	TGCGGGCAGTCAGAGATTAACCTATTTAAATGGTATCAGCATTAACCGGAAA	120
Db	64	TGCGGGCAGTCAGAGATTAACCTATTTAAATGGTATCAGCATTAACCGGAAA	123
Qy	121	GCCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGTCCCATCAAGTTTC	180
Db	124	GCCCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGTCCCATCAAGTTTC	183
Qy	181	AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGACCTTGAAGAT	240
Db	184	AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT	243
Qy	241	TTTGCAGTTACTACTGTCAAGAGAGTCTCAGTCCCTCGTACACTTTTGGCCGGGACC	300
Db	244	TTTGCAGTTACTACTGTCAAGAGAGTCTCAGTCCCTCGTACACTTTTGGCCGGGACC	303
Qy	301	AAGTGGGAGATCAACGA	318

Db 304 AAGCTGGAGATCAAAACGA 321
|||||

RESULT 2

US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

Query Match 88.4%; Score 281.2; DB 3; Length 321;
Best Local Similarity 92.8%; Pred. No. 7e-89;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1 GAGCTCACTCACTCCATCTCCCTCTGTCGATCTGCGAGACAGAGTCAACATCACT 60
Db 4 GAGCTCACTCACTCCATCTCCCTCTGTCGATCTGCGAGACAGAGTCAACATCACT 63
Qy 61 TGCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATATAAACCCAGGAAA 120
Db 64 TGCCGGGCAAGTCAGAGCAATAGCAGCTATTAAATTTGGTATCAGCATATAAACCCAGGAAA 123
Qy 121 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTTC 180
Db 124 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTTC 183
Qy 181 AGTGCAGTGTATGGGACAGACTTCACTCTCACCATCAGAGTCTGAGCCTCAAGAT 240
Db 184 AGTGCAGTGTATGGGACAGACTTCACTCTCACCATCAGAGTCTGAGCCTCAAGAT 243
Qy 241 TTTCGAAGTTACTCTGTCAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGGACC 300
Db 244 TTTCGAAGTTACTCTGTCACAGAGTTCACAGTACAGTACCTGTGGACGTTGGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAAAACGA 318
Db 304 AAGGTGGAATCAAAACGA 321

RESULT 3

US-09-240-274-109
; Sequence 109, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11

; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I09
US-09-240-274-109

Query Match 88.4%; Score 281.2; DB 3; Length 321;
Best Local Similarity 92.8%; Pred. No. 7e-89;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1 GAGCTCACTCACTCCATCTCCCTCTGTCGATCTGCGAGACAGAGTCAACATCACT 60
Db 4 GAGCTCACTCACTCCATCTCCCTCTGTCGATCTGCGAGACAGAGTCAACATCACT 63
Qy 61 TGCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATATAAACCCAGGAAA 120
Db 64 TGCCGGGCAAGTCAGAGCAATAGCAGCTATTAAATTTGGTATCAGCATATAAACCCAGGAAA 123
Qy 121 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTTC 180
Db 124 GCCCTTAAGCTCTGATCTATGTCGATCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTTC 183
Qy 181 AGTGCAGTGTATGGGACAGACTTCACTCTCACCATCAGAGTCTGAGCCTCAAGAT 240
Db 184 AGTGCAGTGTATGGGACAGACTTCACTCTCACCATCAGAGTCTGAGCCTCAAGAT 243
Qy 241 TTTCGAAGTTACTCTGTCAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGGACC 300
Db 244 TTTCGAAGTTACTCTGTCACAGAGTTCACAGTACAGTACCTGTGGACGTTGGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAAAACGA 318
Db 304 AAGGTGGAATCAAAACGA 321

RESULT 4

US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-218

Query Match 88.4%; Score 281.2; DB 3; Length 321;
Best Local Similarity 92.8%; Pred. No. 7e-89;
Matches 295; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
Qy 1 GAGCTCACTCACTCCATCTCCCTCTGTCGATCTGCGAGACAGAGTCAACATCACT 60
Db 4 GAGCTCACTCACTCCATCTCCCTCTGTCGATCTGCGAGACAGAGTCAACATCACT 63
Qy 61 TGCCGGGCAAGTCAGAGAAATTAACACCTATTAAATTTGGTATCAGCATATAAACCCAGGAAA 120

Db 64 TCGCGGCAAGCTCAGAGCATTTAGCAGCTATTATAATTGGTATCAGCAGAAACCAAGGAAA 123
Qy 121 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGGTCCCATCAAGGTTT 180
Db 124 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGGTCCCATCAAGGTTT 183
Qy 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCACSCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACACCTGAAGAT 243
Qy 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTACACTTTTGGCCAGGGGACC 300
Db 244 TTTCGAAGTTACTACTGTCAAGAGAGTTACAGTACCCCGTGGACGTTTCGGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAACGA 318
Db 304 AAGGTGGAGATCAACGA 321

RESULT 5

US-09-240-274-107
; Sequence 107, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I07
US-09-240-274-107

Query Match 87.9%; Score 279.6; DB 3; Length 321;
Best Local Similarity 92.5%; Pred. No. 2.5e-88;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 GAGCTCACTCAGTCTCCATCTCCTCTGTGCTATCTGTGGGACAGAGTCACCATCAGT 60
Db 4 GAGCTCACCAGTCTCCATCTCCTCTGTGCTATCTGTAGGAGACAGATCACCATCACT 63
Qy 61 TCGCGGCAAGCTCAGAGATTAACCACTATTATAATTGGTATCAGCAGAAACCAAGGAAA 120
Db 64 TCGCGGCAAGCTCAGAGATTTAGCAGCTATTATAATTGGTATCAGCAGAAACCAAGGAAA 123
Qy 121 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGGTCCCATCAAGGTTT 180
Db 124 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGGTCCCATCAAGGTTT 183
Qy 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCACSCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACACCTGAAGAT 243
Qy 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTACACTTTTGGCCAGGGGACC 300
Db 244 TTTCGAAGTTACTACTGTCAAGAGAGTTACAGTACCCCGTGGACGTTTCGGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAACGA 318
Db 304 AAGGTGGAGATCAACGA 321

RESULT 6

US-09-240-274-113
; Sequence 113, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I13
US-09-240-274-113

Query Match 87.9%; Score 279.6; DB 3; Length 321;
Best Local Similarity 92.5%; Pred. No. 2.5e-88;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
Qy 1 GAGCTCACTCAGTCTCCATCTCCTCTGTGCTATCTGTGGGACAGAGTCACCATCAGT 60
Db 4 GAGCTCACCAGTCTCCATCTCCTCTGTGCTATCTGTAGGAGACAGATCACCATCACT 63
Qy 61 TCGCGGCAAGCTCAGAGATTAACCACTATTATAATTGGTATCAGCAGAAACCAAGGAAA 120
Db 64 TCGCGGCAAGCTCAGAGATTTAGCAGCTATTATAATTGGTATCAGCAGAAACCAAGGAAA 123
Qy 121 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGGTCCCATCAAGGTTT 180
Db 124 GCCCTTAAGCTCCCTGATCTATGCTGCATCCAGTTTGAAAGTGGGGTCCCATCAAGGTTT 183
Qy 181 AGTGGCAGTGGATATGGGACAGACTTCACTCTCACCATCAGCAGTCTGCACSCCTGAAGAT 240
Db 184 AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCACACCTGAAGAT 243
Qy 241 TTTCGAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCTGTACACTTTTGGCCAGGGGACC 300
Db 244 TTTCGAAGTTACTACTGTCAAGAGATTTACAGTACCCCGTGGACGTTTCGGCCAGGGGACC 303
Qy 301 AAGGTGGAGATCAACGA 318
Db 304 AAGGTGGAGATCAACGA 321

RESULT 7

US-09-240-274-221
; Sequence 221, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; EARLIER FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221

LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-221

Query Match
Best Local Similarity 87.9%; Score 279.6; DB 3; Length 321;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCAACATCACT 60
DB 4 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCAACATCACT 63

QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACAGGAAA 120
DB 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACAGGAAA 123

QY 121 GCGCTAAGCTCCTGATCTATCTGCTGATCCAGTCTTGCAGGTTGCAAGTCCATCAAGGTTTC 180
DB 124 GCGCTAAGCTCCTGATCTATCTGCTGATCCAGTCTTGCAGGTTGCAAGTCCATCAAGGTTTC 183

QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGTCTGAGCTTGAAGTTC 240
DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGTCTGAGCTTGAAGTTC 243

QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 303

QY 301 AAGGTGGAGATCAACAGA 318
DB 304 AAGGTGGAGATCAACAGA 321

RESULT 8
US-09-240-274-222
Sequence 222, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 222
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-222

Query Match
Best Local Similarity 87.9%; Score 279.6; DB 3; Length 321;
Matches 294; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCAACATCACT 60
DB 4 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCAACATCACT 63

QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACAGGAAA 120
DB 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACAGGAAA 123

QY 121 GCCCTAAGCTCCTGATCTATCTGCTGATCCAGTCTTGCAGGTTGCAAGTCCATCAAGGTTTC 180
DB 124 GCCCTAAGCTCCTGATCTATCTGCTGATCCAGTCTTGCAGGTTGCAAGTCCATCAAGGTTTC 183

QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGTCTGAGCTTGAAGTTC 240
DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGTCTGAGCTTGAAGTTC 243

QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 303

QY 301 AAGGTGGAGATCAACAGA 318
DB 304 AAGGTGGAGATCAACAGA 321

RESULT 9
US-09-240-274-201
Sequence 201, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 201
LENGTH: 321
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201

Query Match
Best Local Similarity 86.9%; Score 276.4; DB 3; Length 321;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCAACATCACT 60
DB 4 GAGCTCACTCAGTCCATCCCTCCCTGCTGCTGATCTGTGGGAGACAGAGTCAACATCACT 63

QY 61 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACAGGAAA 120
DB 64 TGCCGGGCAAGTCAGAGATTAACACCTATTAAATTTGGTATCAGCATAAACAGGAAA 123

QY 121 GCCCTAAGCTCCTGATCTATCTGCTGATCCAGTCTTGCAGGTTGCAAGTCCATCAAGGTTTC 180
DB 124 GCCCTAAGCTCCTGATCTATCTGCTGATCCAGTCTTGCAGGTTGCAAGTCCATCAAGGTTTC 183

QY 181 AGTGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGTCTGAGCTTGAAGTTC 240
DB 184 AGTGCAGTGGATATGGGACAGACTTCACTCTCAGCATCAGAGTCTGAGCTTGAAGTTC 243

QY 241 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 300
DB 244 TTTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTGCTACACTTTTGGCCAGGGACC 303

QY 301 AAGGTGGAGATCAACAGA 318
DB 304 AAGGTGGAGATCAACAGA 321

RESULT 10
US-09-240-274-211

```
; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH36
; US-09-240-274-211

Query Match      86.9%; Score 276.4; DB 3; Length 321;
Best Local Similarity 91.8%; Pred. No. 3.4e-87;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
Qy 61 TCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACAGGAAA 120
Db 64 TCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACAGGAAA 123
Qy 121 GCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTT 180
Db 124 TCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTT 183
Qy 181 AGTGGAGTGATATGGACAGATTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGGAGTGATATGGACAGATTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT 243
Qy 241 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 297
Db 244 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 300
Qy 301 AAGTGGAGATCAACGA 318
Db 304 AAGTGGAGATCAACGA 321

RESULT 11
US-09-240-274-101
; Sequence 101, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
; US-09-240-274-112

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 4e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

Qy 1 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
Qy 61 TCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACAGGAAA 120
Db 64 TCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACAGGAAA 123
Qy 121 GCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTT 180
Db 124 GCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTT 183
Qy 181 AGTGGAGTGATATGGACAGATTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGGAGTGATATGGACAGATTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT 243
Qy 241 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 297
Db 244 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 303
Qy 298 ACCAAGTGGAGATCAACGA 318
Db 304 ACCAAGTGGAGATCAACGA 324

RESULT 12
US-09-240-274-112
; Sequence 112, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
; US-09-240-274-112

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 4e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

Qy 1 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
Qy 61 TCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACAGGAAA 120
Db 64 TCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACAGGAAA 123
Qy 121 GCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTT 180
Db 124 GCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTT 183
Qy 181 AGTGGAGTGATATGGACAGATTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGGAGTGATATGGACAGATTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT 243
Qy 241 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 297
Db 244 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 303
Qy 298 ACCAAGTGGAGATCAACGA 318
Db 304 ACCAAGTGGAGATCAACGA 324
```

```
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I01
; US-09-240-274-101

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 4e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

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Db 4 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
Qy 61 TCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACAGGAAA 120
Db 64 TCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACAGGAAA 123
Qy 121 GCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTT 180
Db 124 GCCCTAAGCTCTGTATCTATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTT 183
Qy 181 AGTGGAGTGATATGGACAGATTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT 240
Db 184 AGTGGAGTGATATGGACAGATTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT 243
Qy 241 TTGCAAGTTACTACTCTCAAGAGAGTCTCAGTGCC--TCGTACACTTTTGGCCAGGACC 297
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Qy 298 ACCAAGTGGAGATCAACGA 318
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RESULT 12
US-09-240-274-112
; Sequence 112, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I12
; US-09-240-274-112

Query Match      86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 4e-87;
Matches 300; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

Qy 1 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCACTCAGTCTCCATCTCCTGTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
Qy 61 TCCGGGCAAGTCAGAGATTAACACCTATTAAATTGGTATCAGCATAAACAGGAAA 120
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Qy 298 ACCAAGTGGAGATCAACGA 318
Db 304 ACCAAGTGGAGATCAACGA 324
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RESULT 13

US-09-240-274-210
; Sequence 210, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-240-274-210

Query Match 86.9%; Score 276.2; DB 3; Length 324;
Best Local Similarity 93.5%; Pred. No. 4e-87; Indels 3; Gaps 1;
Matches 300; Conservative 0; Mismatches 18;

QY 1 GAGTCTCACTCAGTCTCCATCTCCTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
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QY 61 TCCCGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATTAACACGGGAAA 120
Db 64 TCCCGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATTAACACGGGAAA 123
QY 121 GCCCTTAAGCTCCTGATCTATGTCATCTCCATCCAGTTTGGAAAGTGGGTCCCATCAAGGTTTC 180
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QY 181 AGTGCAGTGGATATGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 240
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QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGT---GCCTGTACACTTTTGGCCAGGG 297
Db 244 TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG 303
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Db 304 ACCAAGCTGGAGATCAAAACGA 324
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RESULT 14

US-09-240-274-105
; Sequence 105, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:

; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I05
US-09-240-274-105

Query Match 86.4%; Score 274.8; DB 3; Length 321;
Best Local Similarity 91.5%; Pred. No. 1.2e-86;
Matches 291; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1 GAGTCTCACTCAGTCTCCATCTCCTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 60
Db 4 GAGTCTCACTCAGTCTCCATCTCCTCTGTCATCTGTGGAGACAGAGTCACCATCAGT 63
QY 61 TCCCGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATTAACACGGGAAA 120
Db 64 TCCCGGCAAGTCAGAGATTAACACCTATTTAAATTTGGTATCAGCATTAACACGGGAAA 123
QY 121 GCCCTTAAGCTCCTGATCTATGTCATCTCCATCCAGTTTGGAAAGTGGGTCCCATCAAGGTTTC 180
Db 124 GCCCTTAAGCTCCTGATCTATGTCATCTCCATCCAGTTTGGAAAGTGGGTCCCATCAAGGTTTC 183
QY 181 AGTGCAGTGGATATGGACAGACTTCACTCTCACCATCAGCAGTCTGCAGCTCAAGAT 240
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QY 241 TTGCAAGTTACTACTGTCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC 300
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QY 301 AAGTGGAGATCAAAACGA 318
Db 304 AAGTGGAAATCAAAACGA 321
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RESULT 15

US-09-240-274-216
; Sequence 216, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH47
US-09-240-274-216

Query Match 86.4%; Score 274.8; DB 3; Length 321;
Best Local Similarity 91.5%; Pred. No. 1.2e-86;
Matches 291; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy	1	GAGCTCACTCAGTCTCCATCTCCCTCTCTGCACTCTGTGGGAGACAGAGTCACCATCAGT	60
Db	4	GAGTCACCCAGTCTCCATCTCCCTCTCTGCACTCTGTAGGAGACAGAGTCACCATCACT	63
Qy	61	TGCGGGCAAGTCAGAGATTAACACCTATTTAAATTGGTATCAGCATAAACCAGGGAAA	120
Db	64	TGCGGGCAAGTCAGAGCACTAGCACTATTTAAATTGGTATCAGCAGAAACCAGGAAAA	123
Qy	121	GCCCTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTC	180
Db	124	GCCCTAAGTCTCTGATCTATGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTC	183
Qy	181	AGTGGCAGTGGATATGGGACAGACTTCACCTCTACCATCAGCAGTCTGCAGCCTGAAGAT	240
Db	184	AGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAGCCTGAAGAT	243
Qy	241	TTTGCAAGTTACTACTGCAAGAGAGTCTCAGTGCCTCGTACACTTTTGGCCAGGGACC	300
Db	244	TTTGCAACTTACTACTGCAAGAGAGTTCAGTTATCTCGCAGCTTCGGCCAGGGACC	303
Qy	301	AGGTGGAGATCAACGA	318
Db	304	AGGTGGAGATCAGACGA	321

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2004, 19:27:23 ; Search time 1368.2 Seconds
(without alignments)
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Title: US-10-027-725A-5

Perfect score: 318

Sequence: 1 gagctcaccagctccatc.....ccaaactggagatcaaacga 318

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Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

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21: em_ov.*

22: em_pat.*

23: em_ph.*

24: em_pl.*

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26: em_sts.*

27: em_un.*

28: em_vi.*

29: em_hrg.*

30: em_hrg_inv.*

31: em_hrg_inv.*

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41: em_hrg_inv.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	278	87.4	322	9	HUMIGHGD	L03142 Homo sapien
4	278	87.4	326	9	HUMIGHGY	L03160 Homo sapien
5	277	87.1	830	9	AB064095	AB064095 Homo sapi
6	276.4	86.9	321	6	AR160973	AR160973 Sequence
7	276.4	86.9	321	6	AR161027	AR161027 Sequence
8	276.4	86.9	328	9	HUMIGHHC	L03164 Homo sapien
9	273.8	86.1	324	9	AB063929	AB063929 Homo sapi
10	273.8	86.1	324	9	AF107245	AF107245 Homo sapi
11	273.8	86.1	390	9	HSU43773	U43773 Human immu
12	273.8	86.1	828	9	AB064098	AB064098 Homo sapi
13	273.4	86.0	315	6	A68535	A68535 Sequence 51
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15	273.4	86.0	318	12	AF044451	AF044451 Synthetic
16	273.2	85.9	321	6	AR160978	AR160978 Sequence
17	273.2	85.9	321	6	AR160984	AR160984 Sequence
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20	273.2	85.9	321	6	AR161046	AR161046 Sequence
21	273.2	85.9	321	9	HSIGVK16F	X73855 H.sapiens m
22	273.2	85.9	796	9	AB064138	AB064138 Homo sapi
23	272.6	85.7	311	9	HSX98989	X98989 H.sapiens r
24	272.2	85.6	387	12	AF453148	AF453148 Synthetic
25	272.2	85.6	429	9	HUMIGKW	M74019 Homo sapien
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30	271.6	85.4	321	6	AR161050	AR161050 Sequence
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35	271.2	85.3	720	6	BD077368	BD077368 Method of
36	271	85.2	311	9	HSX98987	X98987 H.sapiens r
37	270.6	85.1	324	9	AB095281	AB095281 Homo sapi
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39	270.6	85.1	396	6	E12918	E12918 Human mRNA
40	270.6	85.1	761	9	AB064051	AB064051 Homo sapi
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44	270	84.9	321	6	AR161043	AR161043 Sequence
45	270	84.9	321	6	AR161045	AR161045 Sequence

ALIGNMENTS

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LOCUS
DEFINITION Homo sapiens partial mRNA for immunoglobulin kappa light chain
variable region (IGKV gene), clone 60.
ACCESSION AJ458380
VERSION AJ458380.1 GI:20387059
KEYWORDS IGKV gene; immunoglobulin kappa; light chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Flicker,S., Steinberger,P., Norderhaug,L., Sperr,W.R., Majlesi,Y.,
Valent,P., Kraft,D. and Valenta,R.


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QY      301  AAACTGGAGATCAAAACGA 318
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LOCUS      Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ
DEFINITION      region, partial cds, clone:K54.
ACCESSION      AB064095
VERSION      AB064095.1 GI:21669396
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
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Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
Miura,K. and Kurosawa,Y.
TITLE      Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 830)
AUTHORS      Kurosawa,Y.
TITLE      Direct Submission
JOURNAL      Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyoake 470-1192, Japan
(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT      Please visit our web site
FEATURES      URL:http://www.fujita-hu.ac.jp/immunity/.
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QY      2 AGTCAACCCAGTCTCCATCCTCCTGTCTGTAGGACAGAGTCACCATCACTT 61

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Db      254  GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT 313
QY      242  TTGCAAGTTACTACTGTCGAACAGAGTTACACTTATATACCTTTCGGCCTGGACCA 301
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QY      302  AACTGGAGATCAAAACGA 318
Db      374  AAGTGGATATCAAAACGA 390

RESULT 6
LOCUS      ARI60973      321 bp DNA linear PAT 17-OCT-2001
DEFINITION      Sequence 102 from patent US 6255455.
ACCESSION      ARI60973
VERSION      ARI60973.1 GI:16226189
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 321)
AUTHORS      Siegel,D.L.
TITLE      Rh(D)-binding proteins and magnetically activated cell sorting
method for production thereof
JOURNAL      Patent: US 6255455-A 102 03-JUL-2001;
FEATURES      Location/Qualifiers
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Query Match      86.9%; Score 276.4; DB 6; Length 321;
Best Local Similarity 91.8%; Pred. No. 7.7e-78;
Matches 292; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Db      244  TTTCGAAGTTACTACTGTCGAACAGAGTTACACTTATATACCTTTCGGCCTGGACC 303
QY      301  AAACTGGAGATCAAAACGA 318
Db      304  AAGTGGATATCAAAACGA 321

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JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 324)
 AUTHORS Kurosawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
 COMMENT (E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)
 Please visit our web site
 URL: http://www.fujita-hu.ac.jp/immunity/
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ORIGIN

Query Match 86.1%; Score 273.8; DB 9; Length 324;
 Best Local Similarity 91.5%; Pred. No. 5,3e-77;
 Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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 DB 8 AGATGACCCAGTCTCCATCCCTGCTGCTGTAGGAGACAGATCACCATCACTT 67
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 QY 62 GCCGGGCAGTCAGAGTATTAGCAGCTATTAAATTGGTATCAGCAGAAACCGGGAAG 121
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 DB 68 GCCGGGCAGTCAGAGCAATTAGCAGCTATTAAATTGGTATCAGCAGAAACCGGGAAG 127
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 QY 122 CCCCTAAGCTCTGATCTGTAGTGCATCCAAATTTGCCAAAGTGGGTCCCATCCAGGTTCA 181
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 DB 128 CCCCTAAGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGTTCA 187
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 QY 182 GTGGCAGTGGATCTGGGACAGATTCATCTCACCATCAGCAATCTGCAACTGAAGACT 241
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 QY 302 AACTGGAGATCAAAACGA 318
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 DB 308 AGTGGAGATCAACGA 324

RESULT 10
 AF107245
 LOCUS Homo sapiens clone MD05 immunoglobulin kappa light chain variable
 DEFINITION region mRNA, partial cds.
 ACCESSION AF107245
 VERSION AF107245.1 GI:6492200
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 324)
 AUTHORS Perera, W.S., Moss, M.T. and Urbaniak, S.J.
 TITLE Molecular Characterization Of Anti-RD Antibodies: Antibody Repertoire, Affinity Maturation And Epitope Specificities Unpublished
 JOURNAL
 REFERENCE 2 (bases 1 to 324)
 AUTHORS Perera, W.S., Moss, M.T., Urbaniak, S.J. and Fraser, R.
 TITLE Direct Submission
 JOURNAL Submitted (18-NOV-1998) Academic Transfusion Medicine Unit, Regional Transfusion Centre, Foresterhill Road, Foresterhill, Aberdeen, Scotland AB25 2ZW, UK
 FEATURES
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ORIGIN

Query Match 86.1%; Score 273.8; DB 9; Length 324;
 Best Local Similarity 91.5%; Pred. No. 5,3e-77;
 Matches 290; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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 QY 182 GTGGCAGTGGATCTGGGACAGATTCATCTCACCATCAGCAATCTGCAACTGAAGACT 241
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 DB 188 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT 247
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 QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATACCTTTCGCGCCCTGGGACCA 301
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 DB 248 TTGCAACTTACTGTCAACAGAGTTACAGTACCCCGTACACTTTTGGCCGAGGACCA 307
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 QY 302 AACTGGAGATCAAAACGA 318
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 DB 308 AGTGGAGATCAACGA 324

RESULT 11
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 LOCUS Human immunoglobulin light chain variable region mRNA, cell line
 DEFINITION 13d2, anti-RD, partial cds.
 ACCESSION U43773
 VERSION U43773.1 GI:1353831
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 390)

AUTHORS	Boucher, G., Broly, H. and Lemieux, R.
TITLE	Restricted Use of Cationic Germaline VH Gene Segments in Human Rh (D)
JOURNAL	Red Cell Antibodies
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 390)
TITLE	Boucher, G.
JOURNAL	Direct Submission
REFERENCE	Submitted (21-DEC-1995)
AUTHORS	Gerard Boucher, Research and Development, The Canadian Red Cross Society, Transfusion Center of Quebec, 2535 Laurier Boulevard, Ste-Foy, Quebec G1V 4M3, Canada
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misc_feature	/note="encodes FR2" 214..234
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ORIGIN	

Query Match	86.1%;	Score	273.8;	DB	9;	Length	390;	
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	74	AGATGACCCAGTCTCCATCTCCTCGTGTCTGCATCTGTAGGAGACAGAGTCACCATC	ACTT	133				
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	134	GCCGGGCACTGCAGAGTATTAGCAGTATTATTAATTGGTATCAGCAGAAACCGGGAAG	193					
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Db								
	194	CCCTTAGGCTCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCCAGGTTC	A	253				
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	254	GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAAGTT	313					
QY	242	TTGCAAGTTACTACTGTCAACAGAGTTTACACTACCTTATATACCTTCGGCCCTGGGACCA	301					
Db								
	314	TTGCAGTTACTACTGTCAACAGAGTTTACATACCCCTATTCACTTCGGCCCTGGGACCA	373					
QY	302	AATCGAGATCAAAACGA	318					

Db	374	AAGTGGATATCAACGA	390	
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AB064098				
LOCUS	AB064098	828 bp	mRNA	linear
DEFINITION	Homo sapiens IGH mRNA for immunoglobulin kappa light chain VLJ region, partial cds, clone:K57.			
ACCESSION	AB064098			
KEYWORDS	AB064098.1	GI:21669402		
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1. Akahori Y., Iba Y., Morino K., Shinochara M., Hirono Y., Kakita M., Suzuki K., Torii H., Ukai Y., Honda T., Katsumi H., Okada J., Mura K. and Kurosawa Y.			
TITLE	Construction and characterization of antibody libraries: isolation of the therapeutic human antibodies and application to functional genomics			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 828)			
AUTHORS	Kurosawa Y.			
TITLE	Direct Submission			
JOURNAL	Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan			
COMMENT	(E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387) Please visit our web site			
FEATURES	URL:http://www.fujita-hu.ac.jp/immunity/. Location/Qualifiers			
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				SOURCE

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Db	74	AGATGACCCAGTCTCCATCCTCTCCCTGTCCTGTAGGACACAGATCACCATCACTT	133			
QY	62	GCGGGACGTCAGAGTATTACACCTATTTAAATTGGTATCAGCAGAAACGGGGAGG	121			
Db	134	GCGGGCAGTTCAGAGCATTAGCGCTATTTAAATTGGTATCAGCAGAAACGAGGGAAG	193			
QY	122	CCCTAAGCTCTGTATCTAGTGCATCCAAATTTCGMAAGTGGGGTCCCATCCAGGTTC	181			

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QY      182  GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
Db      254  GTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT 313
QY      242  TTGCAAGTACTACTGTCAACAGAGTTACACTTACCTTATATACCTTCGGCCCTGGGACCA 301
Db      314  TTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGACCTTTTGGCCAGGGGACCA 373
QY      302  AACTGGAGATCAACGA 318
Db      374  AGCTGGAGATCAACGA 390

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RESULT 13
LOCUS   A68535
DEFINITION
Sequence 51 from Patent WO9749809.
ACCESSION
A68535
VERSION
A68535.1 GI:4759587
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Miescher, S., Vogel, M., Stadler, B., Morell, A., Imboden, M. and
Amstutz, H.
TITLE
POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING STRUCTURES WITH
SPECIFICITY FOR THE RHESUS D ANTIGENS. THE DNA ENCODING THEM AND
THE PROCESS FOR THEIR PREPARATION AND USE
JOURNAL
Patent: WO 9749809-A 51 31-DEC-1997;
ROTKREUZSTIFTUNG ZENTRALLAB (CH)
FEATURES
Location/Qualifiers
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Query Match      86.0%; Score 273.4; DB 6; Length 315;
Best Local Similarity 91.7%; Pred. No. 7.2e-77;
Matches 289; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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ORIGIN

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Best Local Similarity 91.7%; Pred. No. 7.2e-77;
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Db      301  AAAGTGGATCAAA 315

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RESULT 14
LOCUS   HSLD220VL
DEFINITION
H. sapiens mRNA for variable region of immunoglobulin kappa light
chain, clone LD2-20-VL.
ACCESSION
Y08251
VERSION
Y08251.1 GI:1561609
KEYWORDS
Ig kappa chain; immunoglobulin; light chain; variable region.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Miescher, S.M.
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 315)
AUTHORS
Miescher, S.M.
TITLE
Direct Submission
JOURNAL
Submitted (19-SEP-1996) S.M. Miescher, Institute of Immunology and
Allergyology, University of Bern, Sahli Haus 2, Inselspital, CH-3010
Bern, SWITZERLAND
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FEATURES

source

source

CDS

ORIGIN

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Query Match      86.0%; Score 273.4; DB 9; Length 315;
Best Local Similarity 91.7%; Pred. No. 7.2e-77;
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Qy 241 TTTCAGAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTCGGGCCCTGGGACC 300
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Qy 301 AAAGTGGAGATCAAA 315
Db 301 AAAGTGGAGATCAAA 315

RESULT 15
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LOCUS AF044451 318 bp mRNA linear SYN 31-OCT-2001
DEFINITION Synthetic construct from Homo sapiens clone I02 anti-Rh(D) antibody
v kappa segment mRNA, partial cds.
ACCESSION AF044451
VERSION AF044451.1 GI:3046473
KEYWORDS .
SOURCE .
ORGANISM .
synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 318)
AUTHORS Siegel,D.L., Chang,T.Y., Russell,S.L. and Bunya,V.Y.
TITLE Isolation of cell surface-specific human monoclonal antibodies
using phage display and magnetically-activated cell sorting:
applications in immunohematology
J. Immunol. Methods 206 (1-2), 73-85 (1997)
97469098
PUBMED 9328570
REFERENCE 2 (bases 1 to 318)
AUTHORS Chang,T.Y. and Siegel,D.L.
TITLE Genetic and immunological properties of phage-displayed human
anti-Rh(D) antibodies: implications for Rh(D) epitope topology
Blood 91 (8), 3066-3078 (1998)
98200617
PUBMED 9531621
REFERENCE 3 (bases 1 to 318)
AUTHORS Chang,T.Y., Russell,S.L., Bunya,V.Y. and Siegel,D.L.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1998) Path & Lab Med, University of Pennsylvania,
36th & Hamilton, Philadelphia, PA 19104, USA
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Qy 121 GCCCTAAGCTCCGTGATCTGTAGTGCATCCAAATTTCGAAAGTGGGTCCCATCCAGGTTTC 180
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Qy 181 AGTGGCAGTGGATCTGGGACAGAGTTTCACTCTCACCATCAGCAATCTGCAACCTTGAAGAC 240
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Qy 301 AAAGTGGAGATCAAA 315
Db 304 AAGGTGGAATCAAA 318

Search completed: August 13, 2004, 03:58:03
Job time : 1369.2 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 00:12:28 ; Search time 1864.96 Seconds
(without alignments)
5091.898 Million cell updates/sec

Title: US-10-027-725A-5

Perfect score: 318

Sequence: 1 gagctcaccagctccatc.....ccaaactggagatcaaacga 318

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estma:*

5: em_estov:*

6: em_estro:*

7: em_estro:*

8: em_hcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vit:*

21: em_gss_fun:*

22: em_gss_nam:*

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27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	270.6	85.1	1084	14	CB986592
3	269	84.6	493	10	AW405753
4	269	84.6	624	14	CD690145

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	269	84.6	770	12	BG685444
6	269	84.6	797	14	CB987347
7	267.4	84.1	525	14	CD705928
8	267.4	84.1	750	14	CB985395
9	265.8	83.6	431	10	AW406886
10	265.8	83.6	693	14	CD684441
11	265.8	83.6	799	14	CB984750
12	265.8	83.6	819	14	CB985931
13	265.8	83.6	864	12	BG548281
14	265.8	83.6	933	13	BQ899146
15	265.8	83.6	992	13	BQ708832
16	264.2	83.1	391	10	AW404992
17	264.2	83.1	447	10	AW405752
18	264.2	83.1	487	10	AW405301
19	264.2	83.1	498	14	CD684450
20	264.2	83.1	499	14	CD685478
21	264.2	83.1	608	10	AW404714
22	264.2	83.1	619	14	CD693603
23	264.2	83.1	724	14	CB959008
24	264.2	83.1	745	14	CB958128
25	264.2	83.1	748	14	CB956867
26	262.8	82.6	471	10	AW406294
27	262.6	82.6	550	14	CD709957
28	262.6	82.6	708	14	CB956923
29	262.6	82.6	725	14	CB987519
30	262.6	82.6	742	14	CB984723
31	262.6	82.6	923	13	BQ882857
32	261.8	82.3	921	12	BG341239
33	261.2	82.1	1067	13	BX397739
34	261	82.1	598	14	CD692150
35	261	82.1	671	12	BM830977
36	261	82.1	684	12	BM769909
37	261	82.1	753	14	CB955708
38	261	82.1	855	14	CB995312
39	259.4	81.6	460	10	AW405906
40	259.4	81.6	532	12	BM823145
41	259.4	81.6	566	10	AW406081
42	259.4	81.6	743	14	CB957909
43	259.4	81.6	754	14	CB986767
44	259.4	81.6	762	14	CB958057
45	259.4	81.6	793	14	CB987506

ALIGNMENTS

RESULT 1
AW407904
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AW407904
UI-HF-BL0-add-a-01-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061128 5', mRNA sequence.
AW407904
AW407904.1 GI:6926961
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/JLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

AW407904
UI-HF-BL0-add-a-01-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3061128 5', mRNA sequence.
AW407904
AW407904.1 GI:6926961
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 422)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/JLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M13 Forward.
 Location/Qualifiers
 1. 493
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3057290"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH MGC 37"
 /note="Vector: p7T3-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

FEATURES source

Query Match 84.6%; Score 269; DB 10; Length 493;
 Best Local Similarity 90.5%; Pred. No. 9, 7e-71;
 Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2 AGCTACCCAGTCTCCATCTCCCTGCTGCTGCTGTAGGAGACAGATCAACATCACTT 61
 Db 79 AGATGACCCAGTCTCCATCTCCCTGCTGCTGCTGTAGGAGACAGATCAACATCACTT 138
 Qy 62 GCCGGGACGTCAGAGTATTAGCACCTATTAAATTGGTATCAGAGAAACCGGGAGG 121
 Db 139 GCCGGGACGTCAGAGTATTAGCACCTATTAAATTGGTATCAGAGAAACCGGGAGG 198
 Qy 122 CCCCTAAGCTCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTCA 181
 Db 199 CCCCTAAGCTCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTCA 258
 Qy 182 GTGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
 Db 259 GTGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGATT 318
 Qy 242 TTGCAAGTTACTACTGTCACAGAGTTACACTATATATACCTTCGGCCCTGGGACCA 301
 Db 319 TTGCAAGTTACTACTGTCACAGAGTTACACTATATACCTTCGGCCCTGGGACCA 378
 Qy 302 AACTGGAGATCAACGA 318
 Db 379 AGGTGGAATCAACGA 395

RESULT 4
 CD690145
 LOCUS 624 bp mRNA linear EST 25-JUN-2003
 DEFINITION EST6668 human nasopharynx Homo sapiens cDNA, mRNA sequence.
 ACCESSION CD690145
 VERSION CD690145.1 GI:32210615
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and
 Zeng, Y.-X.
 JOURNAL Transcriptional Gene Expression Profile of Human Nasopharynx
 COMMENT Unpublished (2003)
 CONTACT: Yixin Zeng
 Cancer Center
 Sun Yat-sen University

651 DongFeng Road East, GuangZhou 510060, China
 Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzeng@gzsums.edu.cn.

FEATURES source

1. 624
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="normal nasopharynx"
 /clone_lib="human nasopharynx"
 /note="TESTS generated from a normal nasopharynx cDNA
 library from southern Chinese"

ORIGIN

Query Match 84.6%; Score 269; DB 14; Length 624;
 Best Local Similarity 90.5%; Pred. No. 1.1e-70;
 Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2 AGCTACCCAGTCTCCATCTCCCTGCTGCTGCTGTAGGAGACAGATCAACATCACTT 61
 Db 121 AGATGACCCAGTCTCCATCTCCCTGCTGCTGCTGTAGGAGACAGATCAACATCACTT 180
 Qy 62 GCCGGGACGTCAGAGTATTAGCACCTATTAAATTGGTATCAGAGAAACCGGGAGG 121
 Db 181 GCCGGGACGTCAGAGTATTAGCACCTATTAAATTGGTATCAGAGAAACCGGGAGG 240
 Qy 122 CCCCTAAGCTCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTCA 181
 Db 241 CCCCTAAGCTCTGATCTGTAGTGCATCCCAATTTGCAAGTGGGTCCCATCCAGGTTCA 300
 Qy 182 GTGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGACT 241
 Db 301 GTGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACCTGAAGATT 360
 Qy 242 TTGCAAGTTACTACTGTCACAGAGTTACACTATATACCTTCGGCCCTGGGACCA 301
 Db 361 TTGCAAGTTACTACTGTCACAGAGTTACACTATATACCTTCGGCCCTGGGACCA 420
 Qy 302 AACTGGAGATCAACGA 318
 Db 421 AGCTGGAGATCAACGA 437

RESULT 5
 BG685444
 LOCUS 602637305F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765129 5',
 DEFINITION mRNA sequence.

ACCESSION BG685444
 VERSION BG685444.1 GI:13916941
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapps-f@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLC1623 row: i column: 02
 High quality sequence stop: 713.
 Location/Qualifiers
 1. 770

FEATURES source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4765129"
/tissue="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 84.6%; Score 269; DB 12; Length 770;
Best Local Similarity 90.5%; Pred. No. 1.3e-70;
Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCTCCCTGCTGTGCTGTAGGACAGAGTCCATCACTT 61
DB |||||
QY 80 AGATGACCAGTCTCCAACTCCCTGCTGTGCTGTAGGACAGAGTCCATCACTT 139
DB |||||
QY 62 GCCGGGACGTCAGAGTATAGCAGCTATTTAAATGGTATCAGCAGAAACCGGGAAG 121
DB |||||
QY 140 GCCGACAGAGTCAGAGATTTAGCAGCTATTTCAATGGTATCAGCAGAAACCGGGAAG 199
DB |||||
QY 122 CCCCTAAGCTCTGATCTGTAGTGATCCAAATTTGCAAGTGGGTGCCATCCAGGTTCA 181
DB |||||
QY 200 CCCCTAAGCTCTGATCTGTGATCCAAATTTGCAAGTGGGTGCCATCCAGGTTCA 259
DB |||||
QY 182 GTGGCAGTGGATCTGGGACAGAGTTCATCTCACCATCAGCATCTGCAACCTGAAGT 241
DB |||||
QY 260 GTGGCAGTGGATCTGGGACAGAGTTCATCTCACCATCAGCATCTGCAACCTGAAGT 319
DB |||||
QY 242 TTGCAAGTCTACTGTCAGCAGAGTTACATCTATACCTTATACCTTCGGCCCTGGGACCA 301
DB |||||
QY 320 TTGCAAGTCTACTGTCAGCAGAGTTACATCTATACCTTATACCTTCGGCCCTGGGACCA 379
DB |||||
QY 302 AACTGGAGATCAAAACGA 318
DB |||||
QY 380 AAGTGGATATCAAAACGA 396
DB |||||

RESULT 6

CB987347
LOCUS
DEFINITION
AGENCOURT 13591809 NIH MGC 184 Homo sapiens cDNA clone
IMAGE:30326300 5', mRNA sequence.

CB987347
VERSION
KEYWORDS
SOURCE

EST.
Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 797)

NIH-MGC <http://imgc.ncbi.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-1@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: NDCM133 row: h column: 21

High quality sequence stop: 437.

FEATURES

source

1..797
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30326300"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
SfiI (ggccctatggcc); Site_2: SfiI (ggccctcggcc); cDNA
library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyroid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 84.6%; Score 269; DB 14; Length 797;
Best Local Similarity 90.5%; Pred. No. 1.3e-70;
Matches 287; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCTCCCTGCTGTGCTGTAGGACAGAGTCCATCACTT 61
DB |||||
QY 106 AGATGACCAGTCTCCATCTCCCTGCTGTGATCTGTAGGACAGAGTCCATCACTT 165
DB |||||
QY 62 GCCGGGACGTCAGAGTATTAGCAGCTATTTAAATGGTATCAGCAGAAACCGGGAAG 121
DB |||||
QY 166 GCCGGGACGTCAGAGTATTAGCAGCTATTTAAATGGTATCAGCAGAAACCGGGAAG 225
DB |||||
QY 122 CCCCTAAGCTCTGATCTGTAGTGATCCAAATTTGCAAGTGGGTGCCATCCAGGTTCA 181
DB |||||
QY 226 CCCCTAAGCTCTGATCTGTAGTGATCCAAATTTGCAAGTGGGTGCCATCCAGGTTCA 285
DB |||||
QY 182 GTGGCAGTGGATCTGGGACAGAGTTCATCTCACCATCAGCATCTGCAACCTGAAGT 241
DB |||||
QY 286 GTGGCAGTGGATCTGGGACAGAGTTCATCTCACCATCAGCATCTGCAACCTGAAGT 345
DB |||||
QY 242 TTGCAAGTCTACTGTCAGCAGAGTTACATCTATACCTTATACCTTCGGCCCTGGGACCA 301
DB |||||
QY 346 TTGCAAGTCTACTGTCAGCAGAGTTACATCTATACCTTATACCTTCGGCCCTGGGACCA 405
DB |||||
QY 302 AACTGGAGATCAAAACGA 318
DB |||||
QY 406 AAGTGGATATCAAAACGA 422
DB |||||

RESULT 7

CD705928
LOCUS
DEFINITION
EST22455 human nasopharynx Homo sapiens cDNA, mRNA sequence.

CD705928
VERSION
KEYWORDS
SOURCE

EST.
Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 525)

Liu.X.-Q., Zhou.Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and

Zeng,Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)

Contact: Yixin Zeng

Cancer Center

Sun Yat-sen University

651 DongFeng Road East, GuangZhou 510060, China

Tel: 86-1380-9770-743
 Fax: 86-20-8775-4506
 Email: yxzen@gzsums.edu.cn.
 Location/Qualifiers
 1..525
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="normal nasopharynx"
 /clone_lib="human nasopharynx"
 /note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

FEATURES

source

ORIGIN

Query Match 84.1%; Score 267.4; DB 14; Length 525;
 Best Local Similarity 90.2%; Pred. No. 3.1e-70;
 Matches 286; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCCCTCTGCTGTAGGACACAGAGTCACCATCACTT 61
 |||
 Db 124 AGATGACCCAGTCTCCATCCCTCTGCTGTAGGACACAGAGTCACCATCACTT 183
 |||

QY 62 GCCGGGACGTCAGAGTATTAGCCTATTTAAATTGGTATCAGCAGAAACGGGGAAG 121
 |||
 Db 184 GCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCGGGAAG 243
 |||

QY 122 CCCCTAAGCTCTGATCTGTAGTCATCCAAATTCGAAAGTGGGTCCCATCCAGTTCA 181
 |||
 Db 244 CCCCTAAGCTCTGATCTGTAGTCATCCAGTTTCGAAAGTGGGTCCCATCCAGTTCA 303
 |||

QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGACT 241
 |||
 Db 304 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCGCCATCAGCAGCTGCAACTGAAGATT 363
 |||

QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTGGCCCTGGGACCA 301
 |||
 Db 364 TTGCAACTTACCACTGTCAACAGAGTTACAGTACGCCGTACACTTTTGGCCAGGACCA 423
 |||

QY 302 AACTGGAGATCAAAAGCA 318
 |||
 Db 424 ACTTGGAGATCAAAAGCA 440
 |||

RESULT 8
 CB985395
 LOCUS
 DEFINITION AGENCOURT_13643437 NIH_MGC_184 Homo sapiens cDNA clone
 IMAGE:30328513 5', mRNA sequence.
 CB985395
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LML at:
 http://image.llnl.gov
 Plate: NDCM139 row: e column: 02
 High quality sequence stop: 555.
 Location/Qualifiers
 1..750
 /organism="Homo sapiens"

FEATURES

source

/mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30328513"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_184"
 /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
 SfiI (ggccattatggcc); Site_2: SfiI (ggccctcgcc);
 Library is oligo-dT primed and directionally cloned. cDNA
 was prepared from a glandular pool of tissues from thyroid,
 parathyroid, adrenal, cortex and pineal gland. 5' and 3',
 adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGGAGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.38
 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 84.1%; Score 267.4; DB 14; Length 750;
 Best Local Similarity 90.2%; Pred. No. 3.8e-70;
 Matches 286; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCCCTCTGCTGTAGGACACAGAGTCACCATCACTT 61
 |||
 Db 104 AGATGACCCAGTCTCCATCCCTCTGCTGTAGGACACAGAGTCACCATCACTT 163
 |||

QY 62 GCCGGGACGTCAGAGTATTAGCCTATTTAAATTGGTATCAGCAGAAACCGGGAAG 121
 |||
 Db 164 GCCGGGACGTCAGAGTATTAGCCTATTTAAATTGGTATCAGCAGAAACCGGGAAG 223
 |||

QY 122 CCCCTAAGCTCTGATCTGTAGTCATCCAAATTCGAAAGTGGGTCCCATCCAGTTCA 181
 |||
 Db 224 CCCCTAAGCTCTGATCTGTAGTCATCCAGTTTTCGAAAGTGGGTCCCATCCAGTTCA 283
 |||

QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAATCTGCAACTGAAGACT 241
 |||
 Db 284 GTGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGCTGCAACTGAAGATT 343
 |||

QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTACCTTATATACCTTGGCCCTGGGACCA 301
 |||
 Db 344 TTGCAACTTACTACTGTCAACAGAGTTACCGTACCCCTCGAAACTTTCGGGAGGAGGACCA 403
 |||

QY 302 AACTGGAGATCAAAAGCA 318
 |||
 Db 404 AGTGGAGATCAAAAGCA 420
 |||

RESULT 9

AW406886

LOCUS

DEFINITION

UI-HF-BL0-adj-b-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone

IMAGE:3061499 5', mRNA sequence.

AW406886

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: M3 Forward.

FEATURES

source

Location/Qualifiers

1. .431

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3061499"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/lab_host="DH10B (LT1)"

/clone_lib="NIH MGC 37"

/note="Vector: pRT3-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 83.6%; Score 265.8; DB 10; Length 431;

Best Local Similarity 89.9%; Pred. No. 8.5e-70;

Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCTCCCTGCTGCTGTAGGACAGAGTCAACATCACTT 61

Db 67 AGATGACCCAGTCTCATCTCCCTGCTGCTGTAGGACAGAGTCAACATCACTT 126

QY 62 GCCGGGACAGTCTGAGTATTTAGCCTATTTAAATTGGTATCAGCAGAAACCGGGAAG 121

Db 127 GCCGGGACAGTCTGAGTATTTAGCCTATTTAAATTGGTATCAGCAGAAACCGGGAAG 186

QY 122 CCCCTAAGTCTCTGATCTGTGATCCAAATTTGCAAGTGGGTCCCATCCAGTTCA 181

Db 187 CCCCTCAGTCTCTGATCTGTGATCCAAATTTGCAAGTGGGTCCCATCCAGTTCA 246

QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACCTCTCACCATCAGCAATCTGCAACCTGAAGACT 241

Db 247 GTGGCAGTGGATCTGGGACAGAGTTCACCTCTCACCATCAGCAATCTGCAACCTGAAGACT 306

QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATATATACCTTCGGCCCTGGGACCA 301

Db 307 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATATATACCTTCGGCCCTGGGACCA 366

QY 302 AACTGAGATCAACGA 318

Db 367 AGGTGGAGATCAACGA 383

RESULT 10

CD684441

LOCUS

DEFINITION

EST361 human nasopharynx Homo sapiens cdna, mRNA sequence.

ACCESSION

CD684441

VERSION

CD684441.1 GI:32199435

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 693)

Author Liu X.-O., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and

Zeng, Y.-X.

Transcriptional Gene Expression Profile of Human Nasopharynx

Unpublished (2003)

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FEATURES

source

Location/Qualifiers

1. .693

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="normal nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cdna

library from southern Chinese"

ORIGIN

Query Match 83.6%; Score 265.8; DB 14; Length 693;

Best Local Similarity 89.9%; Pred. No. 1.1e-69;

Matches 285; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGCTCACCAGTCTCCATCTCCCTGCTGCTGTAGGACAGAGTCAACATCACTT 61

Db 127 AGATGACCCAGTCTCCATCTCCCTGCTGCTGTAGGACAGAGTCAACATCACTT 186

QY 62 GCCGGGACAGTCTGAGTATTTAGCCTATTTAAATTGGTATCAGCAGAAACCGGGAAG 121

Db 187 GCCGGGACAGTCTGAGTATTTAGCCTATTTAAATTGGTATCAGCAGAAACCGGGAAG 246

QY 122 CCCCTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAGTGGGTCCCATCCAGTTCA 181

Db 247 CCCCTAAGTCTCTGATCTGTAGTGCATCCAAATTTGCAAGTGGGTCCCATCCAGTTCA 306

QY 182 GTGGCAGTGGATCTGGGACAGAGTTCACCTCTCACCATCAGCAATCTGCAACCTGAAGACT 241

Db 307 GTGGCAGTGGATCTGGGACAGAGTTCACCTCTCACCATCAGCAATCTGCAACCTGAAGACT 366

QY 242 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATATATACCTTCGGCCCTGGGACCA 301

Db 367 TTGCAAGTTACTACTGTCAACAGAGTTACACTTATATATATACCTTCGGCCCTGGGACCA 426

QY 302 AACTGAGATCAACGA 318

Db 427 AGGTGGAGATCAACGA 443

RESULT 11

CB984750

LOCUS

DEFINITION

AGENCOURT 13574990 NIH_MGC_184 Homo sapiens cdna clone

IMAGE:30326373 5', mRNA sequence.

ACCESSION

CB984750

VERSION

CB984750.1 GI:30279274

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 799)

Author NIH-MGC <http://mgs.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDCM133 row: k column: 22

High quality sequence stop: 412.

Location/Qualifiers

1. .799

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30326373"

FEATURES

source